

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: Dr. Martin Examiner #: 2102 Date: 8/2/98
Art Unit: 31 Phone Number 301- Serial Number: 7117024
Mail Box and Bldg/Room Location: Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Inventors (please provide full names): Earliest Priority Filing Date:

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Please search factors 1, 2, 3, 4, 5, 6, 7, 8, 9

Thank you

Dr. Martin

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM: 1E02 - 703-308-4498
jan.delaval@usdo.gov

BEST AVAILABLE COPY

(WAIT)

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: <u> </u>	NA Sequence (#) <u> </u>	STN <u> </u>
Searcher Phone #: <u> </u>	AA Sequence (#) <u> </u>	Dialog <u> </u>
Searcher Location: <u> </u>	Structure (#) <u> </u>	Questel/Orbit <u> </u>
Date Searcher Picked Up: <u>8/2/98</u>	Bibliographic <u> </u>	Dr. Link <u> </u>
Date Completed: <u>8/2/98</u>	Litigation <u> </u>	Lexis/Nexis <u> </u>
Searcher Prep & Review Time: <u> </u>	Fulltext <u> </u>	Sequence Systems <u> </u>
Clerical Prep Time: <u> </u>	Patent Family <u> </u>	WWW/Internet <u> </u>
Online Time: <u> </u>	Other <u> </u>	Other (specify) <u> </u>

=> fil hcaplus

FILE 'HCAPLUS' ENTERED AT 11:00:09 ON 28 MAY 2003

USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.

PLEASE SEE "HELP USAGETERMS" FOR DETAILS.

COPYRIGHT (C) 2003 AMERICAN CHEMICAL SOCIETY (ACS)

Copyright of the articles to which records in this database refer is held by the publishers listed in the PUBLISHER (PB) field (available for records published or updated in Chemical Abstracts after December 26, 1990), unless otherwise indicated in the original publications. The CA Lexicon is the copyrighted intellectual property of the American Chemical Society and is provided to assist you in searching databases on STN. Any dissemination, distribution, copying, or storing of this information, without the prior written consent of CAS, is strictly prohibited.

FILE COVERS 1997 - 28 May 2003 VOL 138 ISS 23
FILE LAST UPDATED: 27 May 2003 (20030527/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

=> d all tot 143

L43 ANSWER 3 OF 16 HCAPLUS COPYRIGHT 2003 ACS

AN 2003:119474 HCAPLUS

DD 138:316771

TI Construction of modulators of **protein** kinase-associated **signal** transduction by using a hardware-software system comprising information on the three-dimensional structure of the kinase and application to drug screening and drug design

IN Laster, Morris; Toki, Hiro

FA Keryx Biopharmaceuticals, Inc., USA

SO U.S. Pat. Appl. Publ., 29 pp.

CODEN: USXXCO

PT Patent

LA English

IC 1CM C07H011-02

ECL 536023100

CC 7-3 (Enzymes)

Section cross-reference(s): 1

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
FI	US 2003074400	A1	20030424	US 2002-205302	20020726
FFAI	US 2001-207532P	P	20010726		

AB The invention concerns a hardware-software system comprising information on the three-dimensional structure and nature of certain regions in **protein** kinases. The invention also concerns methods for screening for or synthesizing candidate chem. compds. for regulating kinase activity based on this information.

BT **protein** kinase **signal** transduction modulator hardware software; drug screening design **protein** kinase **signal** transduction modulator

IT **Protein** motifs

(A-region; construction of modulators of **protein** kinase-assocd. **signal** transduction by using hardware-software system comprising information on 3-D structure of kinase and application to drug screening and drug design)

IT **Protein** motifs

(B4-B5 region; construction of modulators of **protein**

- kinase-assocd. **signal** transduction by using hardware-software system comprising information on 3-D structure of kinase and application to drug screening and drug design)
- IT **Protein motifs**
(HJ-loop; construction of modulators of **protein** kinase-assocd. **signal** transduction by using hardware-software system comprising information on 3-D structure of kinase and application to drug screening and drug design)
- IT Human.
(anticancer drugs for; construction of modulators of **protein** kinase-assocd. **signal** transduction by using hardware-software system comprising information on 3-D structure of kinase and application to drug screening and drug design)
- IT Intestine, neoplasm
(colon, drug; construction of modulators of **protein** kinase-assocd. **signal** transduction by using hardware-software system comprising information on 3-D structure of kinase and application to drug screening and drug design)
- IT Antitumor agents
Computer application
Computer program
Cytotoxic agents
Molecular modeling
Molecular recognition
Signal transduction, biological
(construction of modulators of **protein** kinase-assocd. **signal** transduction by using hardware-software system comprising information on 3-D structure of kinase and application to drug screening and drug design)
- IT **Information systems**
(data, for 3-D coordinates; construction of modulators of **protein** kinase-assocd. **signal** transduction by using hardware-software system comprising information on 3-D structure of kinase and application to drug screening and drug design)
- IT Cell morphology
(elongation, in drug screening assay; construction of modulators of **protein** kinase-assocd. **signal** transduction by using hardware-software system comprising information on 3-D structure of kinase and application to drug screening and design)
- IT **Optical ROM disks**
(for 3-D coordinates; construction of modulators of **protein** kinase-assocd. **signal** transduction by using hardware-software system comprising information on 3-D structure of kinase and application to drug screening and drug design)
- IT **Computer application**
(graphics; construction of modulators of **protein** kinase-assocd. **signal** transduction by using hardware-software system comprising information on 3-D structure of kinase and application to drug screening and drug design)
- IT Apoptosis
Cell differentiation
Cell migration
Cell proliferation
Metabolism
Phosphorylation, biological
Secretion (process)
(in drug screening assay; construction of modulators of **protein** kinase-assocd. **signal** transduction by using hardware-software system comprising information on 3-D structure of kinase and application to drug screening and drug design)
- IT Prostate gland
(neoplasm, drug; construction of modulators of **protein** kinase-assocd. **signal** transduction by using hardware-software

system comprising information on 3-D structure of kinase and application to drug screening and drug design)

- IT Databases
(of 3-D coordinates; construction of modulators of **protein** kinase-assocd. **signal** transduction by using hardware-software system comprising information on 3-D structure of kinase and application to drug screening and drug design)
- IT Hydration, chemical
(of exposed motifs; construction of modulators of **protein** kinase-assocd. **signal** transduction by using hardware-software system comprising information on 3-D structure of kinase and application to drug screening and drug design)
- IT Phosphorylation, biological
(**protein**, in drug screening assay; construction of modulators of **protein** kinase-assocd. **signal** transduction by using hardware-software system comprising information on 3-D structure of kinase and application to drug screening and drug design)
- IT Conformation
(**protein**; construction of modulators of **protein** kinase-assocd. **signal** transduction by using hardware-software system comprising information on 3-D structure of kinase and application to drug screening and drug design)
- IT Information systems
(**storage**, for 3-D coordinates; construction of modulators of **protein** kinase-assocd. **signal** transduction by using hardware-software system comprising information on 3-D structure of kinase and application to drug screening and drug design)
- IT Drug design
Drug screening
(structure-based; construction of modulators of **protein** kinase-assocd. **signal** transduction by using hardware-software system comprising information on 3-D structure of kinase and application to drug screening and drug design)
- IT Protein motifs
(α -D-region; construction of modulators of **protein** kinase-assocd. **signal** transduction by using hardware-software system comprising information on 3-D structure of kinase and application to drug screening and drug design)
- IT 142008-29-5, **Protein** kinase A
EL: BSU (Biological study, unclassified); BCU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(α -.; construction of modulators of **protein** kinase-assocd. **signal** transduction by using hardware-software system comprising information on 3-D structure of kinase and application to drug screening and drug design)
- IT 9031-44-1, Kinase 140208-17-9, Lyn tyrosine kinase 372092-30-3, **Protein** kinase
EL: PSU (Biological study, unclassified); BCU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(construction of modulators of **protein** kinase-assocd. **signal** transduction by using hardware-software system comprising information on 3-D structure of kinase and application to drug screening and drug design)

L43 ANSWER 1 OF 16 HCAPLUS COPYRIGHT 2003 ACS

AN 2002:833111 HCAPLUS

DI 137:352439

TI Biosequene information storage in binary format as mathematical summary values

IN Omori, Satoshi

PA Japan

SO PCT Int. Appl., 98 pp.

CODEN: PIXXD2

DT Patent
 LA Japanese
 IC ICM 006E017-30
 ICS 012H015-00
 CC 20-5 (History, Education, and Documentation)
 Section cross-reference(s): 3
 FAN.CHT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2002086761	A1	20021031	WO 2002-JP3801	20020417
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BF, BG, BE, BY, BS, CA, CH, CN, CO, CR, CU, CM, DE, DK, DM, DS, EE, ES, FI, GB, GD, GE, GH, GM, HE, HU, ID, IL, IN, IS, KE, KG, KP, KR, KS, LC, LF, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NC, NO, NZ, OM, PE, PL, PT, PQ, PR, RP, SE, SG, SI, SK, SL, TJ, TK, TN, TR, TT, TS, UA, UG, US, UT, VN, YU, ZA, ZM, ZW, AA, AB, AC, AD, AE, AF, AG, AH, AI, AJ, AK, AL, AM, AN, AO, AP, AQ, AR, AS, AT, AU, AV, AW, AX, AY, AZ, BA, BB, BC, BD, BE, BF, BG, BH, BI, BJ, BK, BL, BM, BN, BO, BP, BQ, BR, BS, BT, BU, BV, BW, BX, BY, BZ, CA, CB, CC, CD, CE, CF, CG, CH, CI, CJ, CK, CL, CM, CN, CO, CP, CQ, CR, CS, CT, CU, CV, CW, CX, CY, CZ, DA, DB, DC, DD, DE, DF, DG, DH, DI, DJ, DK, DL, DM, DN, DO, DP, DQ, DR, DS, DT, DU, DV, DW, DX, DY, DZ, EA, EB, EC, ED, EE, EF, EG, EH, EI, EJ, EK, EL, EM, EN, EO, EP, EQ, ER, ES, ET, EU, EV, EW, EX, EY, EZ, FA, FB, FC, FD, FE, FF, FG, FH, FI, FJ, FK, FL, FM, FN, FO, FP, FQ, FR, FS, FT, FU, FV, FW, FX, FY, FZ, GA, GB, GC, GD, GE, GF, GH, GI, GJ, GK, GL, GM, GN, GO, GP, GQ, GR, GS, GT, GU, GV, GW, GX, GY, GZ, HA, HB, HC, HD, HE, HF, HG, HH, HI, HJ, HK, HL, HM, HN, HO, HP, HQ, HR, HS, HT, HU, HV, HW, HX, HY, HZ, IA, IB, IC, ID, IE, IF, IG, IH, II, IJ, IK, IL, IM, IN, IO, IP, IQ, IR, IS, IT, IU, IV, IW, IX, IY, IZ, JA, JB, JC, JD, JE, JF, JG, JH, JI, JJ, JK, JL, JM, JN, JO, JP, JQ, JR, JS, JT, JU, JV, JW, JX, JY, JZ, KA, KB, KC, KD, KE, KF, KG, KH, KI, KJ, KK, KL, KM, KN, KO, KP, KQ, KR, KS, KT, KU, KV, KW, KX, KY, KZ, LA, LB, LC, LD, LE, LF, LG, LH, LI, LJ, LK, LM, LN, LO, LP, LQ, LR, LS, LT, LU, LV, LW, LX, LY, LZ, MA, MB, MC, MD, ME, MF, MG, MH, MI, MJ, MK, ML, MN, MO, MP, MQ, MR, MS, MT, MU, MV, MW, MX, MY, MZ, NA, NB, NC, ND, NE, NF, NG, NH, NI, NJ, NK, NL, NM, NN, NO, NP, NQ, NR, NS, NT, NU, NV, NW, NX, NY, NZ, OA, OB, OC, OD, OE, OF, OG, OH, OI, OJ, OK, OL, OM, ON, OO, OP, OQ, OR, OS, OT, OU, OV, OW, OX, OY, OZ, PA, PB, PC, PD, PE, PF, PG, PH, PI, PJ, PK, PL, PM, PN, PO, PP, PQ, PR, PS, PT, PU, PV, PW, PX, PY, PZ, QA, QB, QC, QD, QE, QF, QG, QH, QI, QJ, QK, QL, QM, QN, QO, QP, QQ, QR, QS, QT, QU, QV, QW, QX, QY, QZ, RA, RB, RC, RD, RE, RF, RG, RH, RI, RJ, RK, RL, RM, RN, RO, RP, RQ, RR, RS, RT, RU, RV, RW, RX, RY, RZ, SA, SB, SC, SD, SE, SF, SG, SH, SI, SJ, SK, SL, SM, SN, SO, SP, SQ, SR, SS, ST, SU, SV, SW, SX, SY, SZ, TA, TB, TC, TD, TE, TF, TG, TH, TI, TJ, TK, TL, TM, TN, TO, TP, TQ, TR, TS, TT, TU, TV, TW, TX, TY, TZ, UA, UB, UC, UD, UE, UF, UG, UH, UI, UJ, UK, UL, UM, UN, UO, UP, UQ, UR, US, UT, UU, UV, UW, UX, UY, UZ, VA, VB, VC, VD, VE, VF, VG, VH, VI, VJ, VK, VL, VM, VN, VO, VP, VQ, VR, VS, VT, VU, VV, VW, VX, VY, VZ, WA, WB, WC, WD, WE, WF, WG, WH, WI, WJ, WK, WL, WM, WN, WO, WP, WQ, WR, WS, WT, WU, WV, WW, WX, WY, WZ, XA, XB, XC, XD, XE, XF, XG, XH, XI, XJ, XK, XL, XM, XN, XO, XP, XQ, XR, XS, XT, XU, XV, XW, XX, XY, XZ, YA, YB, YC, YD, YE, YF, YG, YH, YI, YJ, YK, YL, YM, YN, YO, YP, YQ, YR, YS, YT, YU, YV, YW, YX, YY, YZ, ZA, ZB, ZC, ZD, ZE, ZF, ZG, ZH, ZI, ZJ, ZK, ZL, ZM, ZN, ZO, ZP, ZQ, ZR, ZS, ZT, ZU, ZV, ZW, ZX, ZY, ZZ				
	JP 2000041528	A1	20001008	JP 2001-120735	20010418
PRAI	JP 2001-120350	A	20010418		
	JP 2001-368001	A	20011130		
	JP 2000-117343	A	20000419		
	JP 2000-149122	A	20000519		
AB	A method and device for storing biosequence information, nucleotide or amino acid sequence, in min. data storage space, by converting text format into binary format, is disclosed. Data are represented by math. summary values. Text data showing the sequences of a column of nucleotides constituting the DNA of a std. sample E are converted into binary data in accordance with a definite conversion rule. Then the binary data are divided into partial data (A(i,j)) of m bits (m.gtoreq.16) having a plural no. of rows and a plural no. of columns. Next, the partial data (A(i,j)) of each row are computed in the non-sequence direction on Galois field GF (2m) to det. the first parity group (B1(i) to B3(i)). Then, the partial data (A(i,j)) of each column are computed in the sequence direction on Galois field GF (2m) to det. the second parity group (C1(j) to C3(j)). From these parity data, the sequences of the nucleotides are approx. represented. Computer readable memory storage devices, such as DVD-ROM, or CD-ROM, are claimed.				
ST	app recording storage sequence computer text binary data conversion;				
	sequence information storage binary format math summary value				
IT	Computers				
	DNA sequences				
	Information, biological				
	Magnetic memory devices				
	Optical ROM disks				
	Protein sequences				
	RNA sequences				
	(Biosequence information storage in binary format as math. summary values)				
IT	Information systems				
	(retrieval, computerized; biosequence information storage in binary format as math. summary values)				
IT	Information systems				
	(storage, computerized; biosequence information storage in binary format as math. summary values)				
IT	Mathematical methods				
	(text to binary data conversion; biosequence information storage in binary format as math. summary values)				
IT	474443-04-9, 1: PN: WO02086761 SEQID: 1 unclaimed RNA 474443-10-2, 1: EN: WO02086761 SEQID: 2 unclaimed DNA				
	FL: PFP (Properties)				
	(unclaimed nucleotide sequence; biosequence information storage in				

binary format as math. summary values)

IT 474443-11-3

PL: FFP (Properties)

(unclaimed **protein** sequence; biosequence information storage
in binary format as math. summary values)

FE.CNT 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD

FE

- (1) Casio Computer Co Ltd; JP 06-162096 A 1994
- (2) Fukuda, M; Dai 22 Kai Joho Kagaku Toronkai Dai 27 Kai Kozo Kassei Sokan
Symposium Koen Yoshishu 1999, F84
- (3) International Business Machines Corp; JP 06-348760 A 1994
- (4) International Business Machines Corp; JP 08-255176 A 1996
- (5) International Business Machines Corp; US 5819268 A 1996
- (6) Mitsubishi Electric Corp; JP 03-63876 A 1991
- (7) Nec Corp; JP 08-320834 A 1996
- (8) Nippon Telegraph & Telephone Corp; JP 09-143472 A 1993
- (9) Robson, B; Computer Applications in Biosciences 1992, P883 HCAPLUS
- (10) Tokyo Electric Co Ltd; JP 04-54656 A 1992

L43 ANSWER 3 OF 16 HCAPLUS COPYRIGHT 2003 ACS

AN 2002:778603 HCAPLUS

DI 137:259621

TI Method and apparatus for improving the performance of microanalytic and
microsynthetic procedures

IN Howard, John K.

PA Matsushita Electric Industrial Co., Ltd., Japan

SO U.S. Pat. Appl. Publ., 9 pp.

CODEN: USMXCO

DT Patent

LA English

IC ICM C12Q001-68

ICS G01N033-53; G01N033-54; G11B007-24; G06F019-00; C12M001-34

DEL 435000000

CC 9-1 (Biochemical Methods)

Section cross-reference(s): 14

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 2002146699	A1	20001010	US 2001-327895	20010409
PRAI	US 2001-327895		20010409		

AB In a first exemplary embodiment, the present invention relates to an app.
for performing an assay comprising a micro-system platform, a CD-ROM
device and an information processor, where the CD-ROM device under control
of the information processor is capable of reading and writing data to the
micro-system platform. The micro-system platform comprises a first
section for storing data in a continuous circular data band, which is
disposed in an inner portion of the micro-system platform, and a second
section including at least one assay, which is formed in an outer portion
of the micro-system platform. During operation, the CD-ROM device
retrieves and stores data related to the performance of the assay in the
circular data band. The information processor is operative for
controlling the CD-ROM device in accordance with the data retrieved from
the circular data band, and for analyzing the results of the assay.

ST app performance microanalysis microsynthetic

IT Disks

(Bioanal.; method and app. for improving performance of microanalytic
and microsynthetic procedures)

IT Interface

(Flat planar; method and app. for improving performance of
microanalytic and microsynthetic procedures)

IT Analysis

(clin.; method and app. for improving performance of microanalytic and
microsynthetic procedures)

IT **Information systems**
 (data; method and app. for improving performance of
 microanalytic and microsynthetic procedures)

IT Aging, animal
 Analytical apparatus
 Diagnosis
 Human
Information systems
Optical ROM disks
Statistical analysis
 (method and app. for improving performance of microanalytic and
 microsynthetic procedures)

IT **Information systems**
 (retrieval; method and app. for improving performance of
 microanalytic and microsynthetic procedures)

IT **Information systems**
 (storage; method and app. for improving performance of
 microanalytic and microsynthetic procedures)

L43 ANSWER 4 OF 16 HCAPLUS COPYRIGHT 2003 ACS
 AN 2002:637867 HCAPLUS
 DI 137:165843
 TI Network for evaluating data obtained in a biochip measurement device
 IN Abraham-fuchs, Klaus; Hengerer, Arne; Gallahue, Kieran T.; Gosch, Greg;
 O'Connell, James P.; Windhab, Norbert
 PA Siemens Aktiengesellschaft, Germany; Nanogen, Inc.
 SO PCT Int. Appl., 18 pp.
 CODEN: PIKXDE
 DT Patent
 LA English
 IC ICM C13Q001-68
 CC 9-16 (Biochemical Methods)
 Section cross-reference(s): 14
 FAN.CIT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2002064826	A2	20020822	WO 2002-EP1565	20020214
	W: CA, JP				
	EW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR				
PEAI	US 2001-784720	A	20010215		

AB In a method and a network for evaluating medical data in a clin. study,
 biochips contg. patient samples with multiple biomol. markers are tested
 in a no. of point of care test devices resp. at point of care sites. Each
 test of each biochip sample produces a diagnostic result, which is entered
 into the electronic patient record for the patient who produced the
 sample. A follow-up examn. is subsequently conducted for each patient,
 and the results of the follow-up examn. are also entered into that
 patient's electronic patient record. The follow-up results indicate
 whether the diagnostic test result was a false pos., a false neg. or
 correct. The follow-up data and the original diagnostic results from all
 point of care sites are electronically transmitted to a remote server,
 which has access to an expert system which uses the test results and the
 follow-up data to automatically devise a measurement protocol for a
 selected pathol.

ST network biochip device

IT **Information systems**
 (Electronic; network for evaluating data obtained
 in a biochip measurement device)

IT Computers
 (Servers; network for evaluating data obtained in a biochip measurement
 device)

IT Clinical analyzers

(biochips; network for evaluating data obtained in a biochip measurement device)

IT Analysis
(clin.; network for evaluating data obtained in a biochip measurement device)

IT Information systems
(data; Medical; network for evaluating data obtained in a biochip measurement device)

IT Information systems
(data; network for evaluating data obtained in a biochip measurement device)

IT Computer application
(expert systems; network for evaluating data obtained in a biochip measurement device)

IT Biochemical molecules
Biomarkers (biological responses)
Communication
Diagnosis
Disease, animal
Human
Memory devices
Samples
(network for evaluating data obtained in a biochip measurement device)

IT Information systems
(network; network for evaluating data obtained in a biochip measurement device)

L43 ANSWER 5 OF 16 HCAPLUS COPYRIGHT 2003 ACS

AN 2002:595322 HCAPLUS

DN 137:121955

TI Systems and computer software products for comparing microarray spot intensities

IN Bartell, Daniel M.; Liu, Wei-min

PA USA

SO U.S. Pat. Appl. Publ., 16 pp.

CODEN: USXKCC

DI Patent

LA English

IC ICM G06F009-00

ICS G06F019-00; G01N033-48; G01N033-50; G06K009-34

NCL 382124000

CC 9-16 (Biochemical Methods)

Section cross-reference(s): 3

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 2002106117	A1	20020808	US 2000-737536	20001213
PRAI	US 2000-737536		20001213		
AB	Methods, systems and computer software products are provided for analyzing gene expression data using pixel intensities.				
ST	system computer software product comparing microarray spot intensity				
IT	Information systems (data; systems and computer software products for comparing microarray spot intensities)				
IT	Gene RL: BSU (Biological study, unclassified); BIOL (Biological study) (expression; systems and computer software products for comparing microarray spot intensities)				
IT	Information systems (storage; systems and computer software products for comparing microarray spot intensities)				
IT	Computer program DNA microarray technology				

Mathematical methods
Memory devices
Microarray technology
Statistical analysis

(systems and computer software products for comparing microarray spot intensities)

- IT Nucleic acids
Oligonucleotides
cDNA
FL: ANT (Analyte); ANST (Analytical study)
(systems and computer software products for comparing microarray spot intensities)
- IT Probes (nucleic acid)
FL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(systems and computer software products for comparing microarray spot intensities)

L43 ANSWER 6 OF 16 HCAPLUS COPYRIGHT 2003 ACS

AN 2002:522146 HCAPLUS

EN 137:59914

TI Database system and method useful for predicting the effect of amino acid substitutions on **protein** structure and stability

IN Edelman, Marvin; Eyal, Eran; Najmanovich, Rafael; Schulev, Vladimir

PA Yeda Research and Development Co. Ltd., Israel

SO ECT Int. Appl., 34 pp.

CODEN: PIKXD2

DT Patent

LA English

IC ICM G01N033-48

CC 9-16 (Biochemical Methods)

Section cross-reference(s): 6

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2002054063	A1	20020711	WO 2001-IL1193	20011114
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BY, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DO, EC, EE, EG, ES, FI, FL, GB, GD, GE, GH, GM, GN, GR, GU, HK, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MY, NA, NC, NE, NG, NI, NL, NO, NP, NZ, OM, PA, PE, PG, PH, PK, PL, PT, QA, RO, RU, SD, SE, SG, SI, SK, SL, SM, SN, SR, ST, SV, TC, TD, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AE, BY, KG				
	FW: GH, GM, KE, LS, MW, MC, SD, SL, SZ, TE, UG, ZM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				

PRAI US 2001-059511P P 20010104

AB A method of predicting an effect of a specific amino acid substitution, or mutation, on a structure or stability of a **protein** of interest is disclosed, as well as hardware for implementing the method. The method is executed, at least in part, by a computer and is effected by (a) selecting at least one pair of structurally characterized **proteins** or portions of **proteins**, members of the at least one pair differing in at least the specific amino acid substitution; and (b) extg. data from the members, the data being useful in predicting the effect of the specific amino acid substitution on at least one structural parameter of at least a portion of the **protein** of interest.

ST database system predicting amino acid substitution **protein** structure stability

IT Computer application

Computer program

Computers

Databases

Information systems

Internet

Memory devices

Molecular orientation

Molecular structure

Optical ROM disks

(database system and method useful for predicting effect of amino acid substitutions on **protein** structure and stability)

IT Amino acids, properties

Proteins

PL: PFP (Properties)

(database system and method useful for predicting effect of amino acid substitutions on **protein** structure and stability)

IT Conformation

(**protein**; database system and method useful for predicting effect of amino acid substitutions on **protein** structure and stability)

IT **Information systems**

(**searching**; database system and method useful for predicting effect of amino acid substitutions on **protein** structure and stability)

RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD

FE

(1) Domingues; Proteins:Structure, Function, and Genetic Suppl 1999, V3, P112

(2) Dubchak; Proceedings of the National Academy of Sciences 1995, V92, P8700 HCAPLUS

(3) Fischer; Protein Science 1996, V5, P947 HCAPLUS

(4) Freire; US 6226603 B1 2001

(5) Hopp; Proceedings of the National Academy of Sciences 1981, V78(6), P3824 HCAPLUS

(6) Parker; Journal of Computer-Aided Molecular Design 1994, V8, P193 HCAPLUS

L43 ANSWER 7 OF 16 HCAPLUS COPYRIGHT 2003 ACS

AN 2002:516579 HCAPLUS

DN 137:59853

TI Remotely programmable matrices with memories

IN Nova, Michael P.; Seryei, Andrew E.

PA Discovery Partners International, Inc., USA

SO U.S., 35 pp., Cont.-in-part of U.S. Ser. No. 429,061.

CODEN: USKHAM

DT Patent

LA English

IC ICM G01N015-06

ICS G01N033-53; G12Q001-08; A61K038-00

NCL 432068100

CC 9-1 (Biochemical Methods)

Section cross-reference(s): 7, 30

FAN.CNT 20

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 6416714	B1	20020709	US 1995-4344-6	19950607
	US 5741462	A	19980421	US 1991-427662	19950425
	US 5874214	A	19990223	US 1991-5373-7	19951003
	US 6025119	A	20000215	US 1991-567746	19951205
	CA 2216645	AA	19961121	CA 1996-2216645	19960425
	WO 9636436	A1	19961121	WO 1996-US6145	19960425
	W:	AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CO, DE, DK, EE, ES, FI, GB, GE, HU, IC, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI			
	RW:	KE, LS, MW, SD, SE, SG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN			
EP	3,2861	A1	19980211	EP 1996-916437	19960425
	R:	AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,			

IE, SI, LT, LV, FI

CN	1181730	A	19990513	CN	1996-193374	19960435
JP	11511238	TL	19940918	JP	1996-530062	19960435
AU	9659185	A1	19961129	AU	1996-59185	19960501
AU	707444	B2	19960708			
US	6100016	A	20000408	US	1996-633410	19960610
US	6319668	E1	20011120	US	1996-669252	19960624
US	6284439	E1	20010901	US	1996-711426	19960903
US	6017446	A	20000125	US	1996-709435	19960906
US	5961927	A	19991006	US	1996-723423	19960930
US	6329139	E1	20011111	US	1997-912996	19970511
US	6340588	E1	20020127	US	1998-51022	19980922
PRAI	US 1996-418662	A2	19950425			
	US 1996-184504	A2	19950607			
	US 1996-473660	A	19950607			
	US 1996-480147	A2	19950607			
	US 1996-480196	A	19950607			
	US 1996-484486	A	19950607			
	US 1996-484504	A2	19950607			
	US 1996-538387	A2	19951003			
	US 1996-567746	A	19951125			
	US 1996-639613	A	19960402			
WO	1996-026143	W	19960423			
US	1996-633410	A2	19960610			
US	1996-669252	A2	19960624			
US	1996-711426	A2	19960903			
US	1996-709435	A2	19960906			
US	1996-723423	A2	19960930			
WO	1996-US15909	A2	19961007			
US	1996-736703	B2	19961007			
US	1996-743984	A2	19961028			
US	1996-741685	B2	19961031			
US	1997-837800	B2	19970122			
US	1997-836253	B2	19970227			
US	1997-945053	B2	19971021			
AB	Combinations, called matrixes with memories, of matrix materials with remotely addressable or remotely programmable recording devices that contain at least one data storage unit are provided. The matrix materials are those that are used in, as supports in solid phase chem. and biochem. syntheses, immunoassays and hybridization reactions. The data storage units are preferably non-volatile antifuse memories. By virtue of this combination, mols. and biol. particles, such as phage and viral particles and cells, that are in proximity or in phys. contact with the matrix combination can be labeled by programming the memory with identifying information and can be identified by retrieving the stored information. Combinations of matrix materials, memories, and linked mols. and biol. materials are also provided. The combinations have a multiplicity of applications, including combinatorial chem., isolation and purifn. of target macromols., capture and detection of macromols. for anal. purposes, selective removal of contaminants, enzymic catalysis, chem. modification and other uses.					
ST	remotely programmable matrixes memory; memory device program app array combinatorial phage library					
IT	Electromagnetic field (as tags; remotely programmable matrixes with memories)					
IT	Chromatographs (columns; remotely programmable matrixes with memories)					
IT	Containers (contg. the matrixes with memories; remotely programmable matrixes with memories)					
IT	Information systems (data; remotely programmable matrixes with memories)					
IT	Immunoassay					

(immunoblotting; remotely programmable matrixes with memories)

IT Analytical apparatus

Antifuses

Combinatorial chemistry

Combinatorial library

Computer application

DNA microarray technology

Immobilization, molecular

Immunoassay

Memory devices

Microtiter plates

Northern blot hybridization

Nucleic acid hybridization

Optical detectors

Particles

Phage display library

Process automation

Solid phase synthesis

Southern blot hybridization

Test tubes

Vials

(remotely programmable matrixes with memories)

IT DNA

Proteins

FNA

FL: ANT (Analyte); CRT (Combinatorial reactant); RCT (Reactant); ANST (Analytical study); CMEI (Combinatorial study); RACT (Reactant or reagent) (remotely programmable matrixes with memories)

IT 9004-70-0, Nitrocellulose

FL: DEV (Device component use); USES (Uses) (remotely programmable matrixes with memories)

RE.CNT 517 THERE ARE 517 CITED REFERENCES AVAILABLE FOR THIS RECORD

RE

- (1) Abadeer; US 5334880 A 1994
- (2) Afeyan; US 5389449 A 1995 HCAPLUS
- (3) Agrafiotis; US 5463564 A 1995
- (4) Akaogi; US 5452251 A 1995
- (5) Aldwin; US 5491074 A 1996 HCAPLUS
- (6) Andrews; US 5099226 A 1992
- (7) Anon; FR 2110030 HCAPLUS
- (8) Anon; FR 2526169
- (9) Anon; FR 2553744
- (10) Anon; EP 420177 A1
- (11) Anon; DE 42130639 A1
- (12) Anon; DE 43063639 A1
- (13) Anon; DE 4310169 A1
- (14) Anon; DE 4313807 A1
- (15) Anon; EP 637750 A2 HCAPLUS
- (16) Anon; EP 637750 A2 HCAPLUS
- (17) Anon; DE 9416270 A1
- (18) Anon; FR 2110030 1972 HCAPLUS
- (19) Anon; DE 2344930 1974
- (20) Anon; FR 2526169 1983
- (21) Anon; FR 2553744 1985
- (22) Anon; EP 0126174 1986 HCAPLUS
- (23) Anon; WO 8603840 1986 HCAPLUS
- (24) Anon; WO 8601302 1988 HCAPLUS
- (25) Anon; WO 8901157 1989 HCAPLUS
- (26) Anon; WO 8908164 1989
- (27) Anon; EP 0378053 1990 HCAPLUS
- (28) Anon; WO 9015070 1990 HCAPLUS
- (29) Anon; EP 0410688 1991
- (30) Anon; EP 0420177 1991

- (31) Anon; WO 9201268 1992
- (32) Anon; WO 9207903 1992 HCAPLUS
- (33) Anon; WO 9209300 1992 HCAPLUS
- (34) Anon; WO 9210041 1992 HCAPLUS
- (35) Anon; WO 9213271 1992
- (36) Anon; EP 0526177 A1 1993
- (37) Anon; EP 0526177 A2 1993
- (38) Anon; EP 0539242 1993
- (39) Anon; EP 0541340 1993 HCAPLUS
- (40) Anon; EP 0554995 1993 HCAPLUS
- (41) Anon; EP 0568215 1993
- (42) Anon; DE 4213065 1993
- (43) Anon; DE 4310169 1993
- (44) Anon; DE 4313807 1993
- (45) Anon; WO 9306121 1993 HCAPLUS
- (46) Anon; DE 9308204 1993
- (47) Anon; WO 9308472 1993 HCAPLUS
- (48) Anon; DE 4306563 1994 HCAPLUS
- (49) Anon; WO 9402634 1994 HCAPLUS
- (50) Anon; WO 9405234 1994 HCAPLUS
- (51) Anon; WO 9408051 1994 HCAPLUS
- (52) Anon; WO 9411353 1994 HCAPLUS
- (53) Anon; WO 9413492 1994
- (54) Anon; WO 9413623 1994 HCAPLUS
- (55) Anon; WO 9414989 1994 HCAPLUS
- (56) Anon; DE 9416279 1994
- (57) Anon; WO 9417208 1994 HCAPLUS
- (58) Anon; WO 9422889 1994 HCAPLUS
- (59) Anon; WO 9426413 1994 HCAPLUS
- (60) Anon; WO 9428434 1994 HCAPLUS
- (61) Anon; EP 0637750 1995 HCAPLUS
- (62) Anon; EP 0640826 1995
- (63) Anon; WO 9500530 1995 HCAPLUS
- (64) Anon; WO 9502566 1995 HCAPLUS
- (65) Anon; WO 9604961 1996 HCAPLUS
- (66) Anon; GB 2306484 1997 HCAPLUS
- (67) Anon; WO 9719958 1997 HCAPLUS
- (68) Anon; WO 9720073 1997 HCAPLUS
- (69) Anon; WO 9720074 1997 HCAPLUS
- (70) Anon; Biochem 1972, V11(5), P942
- (71) Anon; NASATECH 1995
- (72) Anon; Science 1995, V276, P577
- (73) Anon; Scrip 1995, P11
- (74) Anon; <http://www.irori.com/products.html> 1996
- (75) Arenzen; US 5343772 A 1994 HCAPLUS
- (76) Ayers; US 5175183 A 1979 HCAPLUS
- (77) Ayers; US 5178439 A 1979 HCAPLUS
- (78) Bakalash; US 5361385 A 1994
- (79) Baldwin; J Am Chem Soc 1995, V117, P5588 HCAPLUS
- (80) Balint; US 4681870 A 1987 HCAPLUS
- (81) Barany; Int J Peptide Protein Res 1987, V30, P705 HCAPLUS
- (82) Barrett; US 5252743 A 1993 HCAPLUS
- (83) Barrett; US 5451683 A 1995 HCAPLUS
- (84) Barrett; US 5483867 A 1996 HCAPLUS
- (85) Basch; J Immunol Meths 1983, V56, P269 MEDLINE
- (86) Batra; Molecular Immunol 1993, V30(4), P379 HCAPLUS
- (87) Baum; C&EN 1994, P20
- (88) Bayer; US 4908405 A 1990 HCAPLUS
- (89) Bayer; US 5392614 A 1994 HCAPLUS
- (90) Bayer; Chem Pept Proteins 1986, V3, P3 HCAPLUS
- (91) Bayer; In Pept:Chem, Struct Biol, Proc Am Pept Symp, 13th 1994, P156 HCAPLUS
- (92) Bayer; Poly-(Ethylene Glycol) Chem 1992, P325 HCAPLUS

- (93) Bayer; Proc Am Pept Symp, 8th 1983, P87 HCAPLUS
- (94) Beck-Sickinger; Peptide Research 1991, V4(2), P88 HCAPLUS
- (95) Beigel; US 4333073 A 1982
- (96) Beigel; US 5214409 A 1993
- (97) Beigel; US 5238120 A 1993
- (98) Beigel; US 5257011 A 1993
- (99) Beigel; US 5266006 A 1993
- (100) Bell; US 5433337 A 1995 HCAPLUS
- (101) Berg; Innovation Perspect Solid Phase Synth Collect Pap, Int Symp, 1st 1990, P453 HCAPLUS
- (102) Berg; J Am Chem Soc 1983, V111, P8024 HCAPLUS
- (103) Berg; Pept, Proc Eur Pept Symp, 10th P196
- (104) Piebricher; US 4177038 A 1979 HCAPLUS
- (105) Biernat; US 3119099 A 1964
- (106) Bird; US 3784992 A 1972 HCAPLUS
- (107) Birge; US 5228001 A 1993
- (108) Birge; US 5253108 A 1993
- (109) Birge; Ann Rev Phys Chem 1990, V41, P683 HCAPLUS
- (110) Bloom; Electronics Systems Design Magazine 1989, P5
- (111) Boardman; US 5290734 A 1994 HCAPLUS
- (112) Boldt; J Immunol 1973, V113(2), P898 HCAPLUS
- (113) Borman; Chem & Engin News 1996, P29
- (114) Braatz; US 5403750 A 1995 HCAPLUS
- (115) Bradley; US 5136572 A 1992
- (116) Brandt; High-throughput screening: An overview 1995, P21 MEDLINE
- (117) Brenner; Proc Natl Acad Sci USA 1991, V89, P5381 HCAPLUS
- (118) Brigham-Burke; US 5395587 A 1995 HCAPLUS
- (119) Brizzolara; US 5236355 A 1993
- (120) Brizzolara; US 5366733 A 1994 HCAPLUS
- (121) Brown; US 5316901 A 1994 HCAPLUS
- (122) Brown; Oligonucleotides Analogues 1991, P1
- (123) Buechler; US 5089391 A 1992 HCAPLUS
- (124) Buechler; Clin Chem 1992, V38(9), P1675 HCAPLUS
- (125) Burin; J Am Chem Soc 1992, V114, P10997 HCAPLUS
- (126) Burin; Proc Natl Acad Sci USA 1994, V91, P4708 HCAPLUS
- (127) Burgess; J Med Chem 1994, V37, P1915 HCAPLUS
- (128) Butcher; US 4991719 A 1991
- (129) Butz; Peptide Res 1994, V7(1), P20 HCAPLUS
- (130) Campbell; US 5024727 A 1991
- (131) Campbell; US 5005548 A 1991
- (132) Campbell; US 5074318 A 1991
- (133) Campbell; US 5359115 A 1994 HCAPLUS
- (134) Campbell; US 5362899 A 1994 HCAPLUS
- (135) Campbell; US 5420328 A 1995 HCAPLUS
- (136) Campbell; US RE34926 E 1995
- (137) Campbell; J Am Chem Soc 1995, V117, P5351 HCAPLUS
- (138) Carroll; US 4857893 A 1989
- (139) Carroll; US 4981928 A 1990
- (140) Carroll; US 5347263 A 1994
- (141) Chan; US 5120662 A 1992 HCAPLUS
- (142) Chang; US 5326696 A 1994 HCAPLUS
- (143) Chen; US 5381035 A 1995 HCAPLUS
- (144) Chen; J Am Chem Soc 1994, V116, P2661 HCAPLUS
- (145) Cherukuri; US 4952531 A 1990 HCAPLUS
- (146) Cherukuri; US 5043221 A 1991 HCAPLUS
- (147) Cherukuri; US 5047371 A 1991 HCAPLUS
- (148) Cherukuri; US 5256463 A 1993
- (149) Chiang; US 5316971 A 1994 HCAPLUS
- (150) Clackson; Nature 1991, V352, P624 HCAPLUS
- (151) Cody; US 5324483 A 1994 HCAPLUS
- (152) Cohen; US 5270351 A 1993
- (153) Cohen; IEEE Transactions on Electron Devices 1994, V41(5), P721
- (154) Coles; US 5314629 A 1994 HCAPLUS

- (155) Cook; Proc IEEE Bipolar Circuits Technol Meet 1986, P99
- (156) Coupek; US 4171412 A 1979 HCAPLUS
- (157) Cuzzette; US 5200051 A 1993 HCAPLUS
- (158) Crane; US 5092592 A 1992 HCAPLUS
- (159) Cunningham; US 5326443 A 1994 HCAPLUS
- (160) Cuwila; Proc Natl Acad Sci USA 1990, V87, P6378 HCAPLUS
- (161) Clainik; Polym Prepr (Am Chem Soc, Div Polym Chem) 1994, V35(2), P985 HCAPLUS
- (162) Dandekar; US 4787019 A 1988
- (163) Darrow; US 5255680 A 1993
- (164) Darrow; US 5265610 A 1993
- (165) Dattagupta; US 4542102 A 1985 HCAPLUS
- (166) Dattagupta; US 5215899 A 1993 HCAPLUS
- (167) Dave; Anal Chem 1994, V66(22), P1121A
- (168) David; US 4376110 A 1983 HCAPLUS
- (169) Davis; US 5358289 A 1993 HCAPLUS
- (170) Desai; US 5334640 A 1994 HCAPLUS
- (171) Desai; US 5416193 A 1995 HCAPLUS
- (172) Devlin; Science 1990, V249, P404 HCAPLUS
- (173) Dewitt; Drug Develop Res 1994, V23, P116 HCAPLUS
- (174) Dewitt; Proc Natl Acad Sci USA 1993, V90, P6909 HCAPLUS
- (175) Dewitt; Proc Natl Acad Sci USA 1993, V90, P6909 HCAPLUS
- (176) Dillon; US 5335750 A 1995 HCAPLUS
- (177) Ditt; US 5111748 A 1992 HCAPLUS
- (178) Dixit; US 5323812 A 1994 HCAPLUS
- (179) Dixit; US 5329153 A 1994 HCAPLUS
- (180) Domkowski; US 4652528 A 1987
- (181) Dorman; US 4705503 A 1987
- (182) Dorman; Biochemistry 1994, V33(19), P5661 HCAPLUS
- (183) Dower; US 5432018 A 1995 HCAPLUS
- (184) Dower; US 5547839 A 1996 HCAPLUS
- (185) Dower; Chapter 38, Annu Rev Med Chem 1991, V26, P271 HCAPLUS
- (186) Downer; US 4975647 A 1990
- (187) Dulac; Cell 1995, V83, P135 HCAPLUS
- (188) Dumoulin; US 5211165 A 1993
- (189) Dumoulin; US 5241625 A 1993
- (190) Dumoulin; US 5271490 A 1993
- (191) Dumoulin; US 5367808 A 1994
- (192) Dumoulin; US 5377678 A 1995
- (193) Dumoulin; US 5437277 A 1995
- (194) Dumoulin; US 5443066 A 1995
- (195) Dumoulin; US 5445170 A 1995
- (196) Dunlap; Symposium on Affinity Chromatography and Immobilized Biochemicals 1974
- (197) Dunlap, R; Immobilized Biochemicals and Affinity Chromatography, Part I 1974
- (198) D'Hont; US 5351952 A 1994
- (199) Erker; Biotechnology 1995, V13, P351 HCAPLUS
- (200) Eichler; Biochem 1993, V32, P11035 HCAPLUS
- (201) Eimori; US 5442212 A 1995
- (202) Ekins; US 4745872 A 1988 HCAPLUS
- (203) Ekins; US 5171695 A 1993 HCAPLUS
- (204) Ekins; US 5304498 A 1994 HCAPLUS
- (205) Ekins; J Clin Immun 1990, V13(4), P169
- (206) Ellman; US 5285514 A 1994 HCAPLUS
- (207) Engelhardt; US 4781120 A 1973
- (208) Eveleigh; US 4985250 A 1989 HCAPLUS
- (209) Eveleigh; US 4954444 A 1990 HCAPLUS
- (210) Farah; US 5217743 A 1993 HCAPLUS
- (211) Fishman; US 3345443 A 1974 HCAPLUS
- (212) Fodor; US 5324633 A 1994
- (213) Fodor; US 5424186 A 1995 HCAPLUS
- (214) Fodor; US 5489673 A 1996 HCAPLUS

- (215) Fodor; US 5511061 A 1996 HCAPLUS
(216) Fodor; Science 1991, V251, P767 HCAPLUS
(217) Fox; US 4489127 A 1984 HCAPLUS
(218) Fraczek; US 5321704 A 1994
(219) Frank; US 3692498 A 1972 HCAPLUS
(220) Freshney; Culture of Animal Cells A Manual of Basic Technique 1983, P141
(221) Frincke; US 5004606 A 1991 HCAPLUS
(222) Farka; Int J Pept Protein Res 1991, V37, P487 HCAPLUS
(223) Gallop; J Med Chem 1994, V37(9), P1233 HCAPLUS
(224) Gardosi; US 4634512 A 1987
(225) Georger; US 5374591 A 1994 HCAPLUS
(226) Georgiou; US 5348867 A 1994 HCAPLUS
(227) Geysen; J Immunol Meth 1987, V102, P259 HCAPLUS
(228) Giampapa; US 5201728 A 1993 HCAPLUS
(229) Giese; US 4272247 A 1979 HCAPLUS
(230) Giles; US 5023918 A 1991
(231) Gilham; Immobilized Polynucleotides and Nucleic Acids P173
(232) Gnadinger; US 5273927 A 1993 HCAPLUS
(233) Goeddel; US 5023408 A 1993 HCAPLUS
(234) Goldmacher; Bioconjugate Chem 1992, V3, P104 HCAPLUS
(235) Goldsmith; US 5306466 A 1994 HCAPLUS
(236) Gordon; US 5307330 A 1993
(237) Gordon; J Med Chem 1994, V37(10), P1385 HCAPLUS
(238) Gould; US 4438515 A 1984 HCAPLUS
(239) Gray; US 5288612 A 1994 HCAPLUS
(240) Grecksch; US 5033633 A 1991
(241) Greve; IEEE Transactions on Electron Devices 1982, VED-29(4), P719 HCAPLUS
(242) Gu; J Optical Soc Am, Selected Papers on Holographic Storage 1992, V9(11), P1978
(243) Gu; Optics Communications, Selected Papers on Holographic Storage 1992, V93, P213
(244) Guire; US 4973493 A 1990 HCAPLUS
(245) Gustafson; US 5572410 A 1996
(246) Gustin; US 5036096 A 1991
(247) Haarer; Japanese Journal of Applied Physics 1987, V26(Supplement 26-4), P227
(248) Haarer; Proc Int Symp on Optical Memory 1987
(249) Hale; Analytical Biochem 1995, V231, P46 HCAPLUS
(250) Hammond; US 5374718 A 1994 HCAPLUS
(251) Hansen; US 5443953 A 1995 HCAPLUS
(252) Harlow; Antibodies A Laboratory Manual, Chap 14 1983
(253) Hasum; Pept, Proc Eur Pept Symp, 16th 1981, P105 HCAPLUS
(254) Hendrick; US 5053659 A 1991
(255) Hermanson; Chaps 1 and 2, Immobilized Affinity Ligand Techniques 1992
(256) Hesser; US 4588880 A 1986
(257) Hessien; US 5217870 A 1993 HCAPLUS
(258) Hidaka; US 4908094 A 1990
(259) Hilferink; US 5146404 A 1992
(260) Hoeman; US 4990756 A 1991
(261) Hoey; US 5333873 A 1995 HCAPLUS
(262) Hogan; US 5216143 A 1993 HCAPLUS
(263) Hollander; US 5029214 A 1991
(264) Holmes; US 5342974 A 1995 HCAPLUS
(265) Holmes; US 5537681 A 1996 HCAPLUS
(266) Holmes; US 5542974 A 1996 HCAPLUS
(267) Holworth; US 5284481 A 1995
(268) Hong; Optical Engineering 1995, V34(1), P2193
(269) Hopfield; US 5063417 A 1991 HCAPLUS
(270) Houghten; US 4631211 A 1986 HCAPLUS
(271) Houghten; BioTechniques 1992, V13(3), P413 HCAPLUS
(272) Houghten; Nature 1991, V354, P84 HCAPLUS
(273) Houghten; Proc Natl Acad Sci USA 1985, V82, P5131 HCAPLUS

- (274) Howard, H; Immobilized Enzyme, Antigens, Antibodies and Peptides Preparation and Characterization 1975
- (275) Hutchinscn; US 5218189 A 1993
- (276) Ill; Macromolecules 1994, P2778 HCAPLUS
- (277) Ill; Biophys J 1993, V64, P919 HCAPLUS
- (278) Inoue; US 4966983 A 1990
- (279) Isailovic; Videodisc and Optical Memory Systems 1985, Piii
- (280) Ishigaki; US 4783776 A 1981
- (281) Ishihara; US 5113163 A 1993
- (282) Ishikawa; J Immunoassay 1983, V4(3), P209 HCAPLUS
- (283) Ito; US 5384918 A 1995 HCAPLUS
- (284) Ito; Polymeric Materials for Microelectronic Applications: Science and Technology, ACS Symposium Series No 579, Chaps 17 1995, P23 HCAPLUS
- (285) Jakoby, W; Affinity Techniques Enzyme Purification: Part B Methods in Enzymology 1974, V34
- (286) Janda; Proc Natl Acad Sci USA 1994, V91, P19779 HCAPLUS
- (287) Jeong; US 5442584 A 1995
- (288) Johansson; Methods in Enzymology 1976, V44, P659 HCAPLUS
- (289) Jones; US 5113315 A 1993 HCAPLUS
- (290) Jung; Angew Chem Int Ed Engl 1991, V31(4), P367
- (291) Jurisch; US 5308967 A 1994
- (292) Jurisch; Identifikation: kontaktlos via Hochfrequenz, Elektronik 1993, V9, P86
- (293) Jurisch; Identifikation: kontaktlos via Hochfrequenz, Elektronik 1993, V9, P86
- (294) Kabat; Experimental Immunochemistry, Chapter 40 Equilibrium Dialysis, 1961, P715
- (295) Kacian; US 5386024 A 1995 HCAPLUS
- (296) Kaji; "Molecular Design of Epoxy Resins for Microelectronics Packaging," Chap 17 1994
- (297) Katsube; US 5196122 A 1994 HCAPLUS
- (298) Kauert; US 4763881 A 1988 HCAPLUS
- (299) Kennedy; Solid Phase Biochemistry, Analytical and Synthetic Aspects 1983, V7, P253
- (300) Kent; Iss J Chem 1978, V17, P243 HCAPLUS
- (301) Kessler; Angew Chem Int Ed Engl 1993, V32(4), P543
- (302) Ketner; Proc Natl Acad Sci USA 1976, V73(4), P1102 HCAPLUS
- (303) Khrapko; FEBS Letts 1989, V256, P118 HCAPLUS
- (304) Kick; J Med Chem 1995, V38, P1427 HCAPLUS
- (305) Kim; US 4179400 A 1979 HCAPLUS
- (306) Kimura; US 5311039 A 1994 HCAPLUS
- (307) King; US 5401373 A 1995 HCAPLUS
- (308) Kip; US 5105190 A 1991
- (309) Kleine; Immunobiol 1994, V190, P53 HCAPLUS
- (310) Kleinman; Analytical Biochem 1987, V166, P1 HCAPLUS
- (311) Koert; US 5416486 A 1995
- (312) Koreyasu; US 5348705 A 1994
- (313) Krizek; US 5347243 A 1994
- (314) Kwch; Proc Natl Acad Sci USA 1994, V91, P1173 HCAPLUS
- (315) Ladner; US 5239409 A 1993 HCAPLUS
- (316) Ladner; US 5260293 A 1993 HCAPLUS
- (317) Ladner; US 5402484 A 1995 HCAPLUS
- (318) Lake; US 5306645 A 1994
- (319) Lam; US 5382513 1995 HCAPLUS
- (320) Lam; Nature V354, P82 HCAPLUS
- (321) Landt; US 5030907 A 1991
- (322) Langer; US 4657543 A 1987 HCAPLUS
- (323) Langer; US 4779806 A 1988
- (324) Le; US 5064767 A 1991 HCAPLUS
- (325) Lee; US 5258459 A 1993 HCAPLUS
- (326) Lee; US 5283153 A 1994
- (327) Lehn; US 5467184 A 1995 HCAPLUS
- (328) Levin; US 5100626 A 1992

- (339) Lewis; US 5346789 A 1994
- (340) Li; Applied Optics 1994, V33(17), P5764
- (341) Ligler; US 5391403 A 1995 HCAPLUS
- (342) Limisimaque; US 4870574 A 1989
- (343) Ling; US 3867517 A 1975 HCAPLUS
- (344) Liskamp; Angew Chem Int Ed Engl 1994, V33(6), P633
- (345) Loetscher; J Chromatography 1992, V595, P113 HCAPLUS
- (346) Loetscher; J Chromatography 1992, V595, P113 HCAPLUS
- (347) Lowe; US 4562157 A 1985 HCAPLUS
- (348) Maeji; Reactive Polymers 1994, V32, P203 HCAPLUS
- (349) Mage; Eur J Immunol 1981, V11, P228 MEDLINE
- (340) Mage; J Immunol Methods 1977, V15, P47 MEDLINE
- (341) Magel; US 5412592 A 1995
- (342) Mandecki; US 5641634 A 1997 HCAPLUS
- (343) Martin; J Med Chem 1995, V38, P1431 HCAPLUS
- (344) Matthews; US 3939123 A 1976 HCAPLUS
- (345) Maucclair; US 5268371 A 1993 HCAPLUS
- (346) McIntyre; US 4318658 A 1982
- (347) McKeehan; J Cell Biol 1976, V71, P727 HCAPLUS
- (348) Merrifield; US 4006117 A 1977 HCAPLUS
- (349) Merrifield; Biochemistry 1964, V3(9), P1345 HCAPLUS
- (350) Mier; US 5211050 A 1993 HCAPLUS
- (351) Miles; Nature 1968, V219, P186 HCAPLUS
- (352) Milliman; US 5232831 A 1993 HCAPLUS
- (353) Milliman; US 5284747 A 1994 HCAPLUS
- (354) Milliman; US 5292874 A 1994 HCAPLUS
- (355) Milliman; US 5353579 A 1994 HCAPLUS
- (356) Mitchell; J Org Chem 1978, V43(14), P2845 HCAPLUS
- (357) Mitchell; J Org Chem 1978, V43(14), P2845 HCAPLUS
- (358) Mitchell; Tetrahedron Lett 1976, V42, P3795
- (359) Mjalli; Net Sci 1995, V1(1) HCAPLUS
- (360) Mok; US 5438439 A 1995
- (361) Mok; Optics Lett 1993, V18(11), P915 HCAPLUS
- (362) Moran; 31st Annual American Chemical Society Western Regional Meeting & 4th Annual San Diego Biotech Exposition 1995, P117
- (363) Moran; J Am Chem Soc 1995, V117, P10787 HCAPLUS
- (364) Mori; US 5451896 A 1995
- (365) Mullis; US 4683102 A 1987 HCAPLUS
- (366) Munc; US 5044623 A 1991
- (367) Nicolaou; Agnew Chem 1995, V34, P2289 HCAPLUS
- (368) Nicolaou; Agnew Chem 1995, V107(20), P1476
- (369) Nikolaiev; Peptide Research 1992
- (370) Nograd; Medicinal Chemistry: A Biochemical Approach 1985, P388
- (371) Nekiara; Shimadzu Hyoron 1993, V50, P25 HCAPLUS
- (372) Hosaka; US 4133642 A 1979
- (373) Ohki; US 4791285 A 1988
- (374) Ojima; US 4908813 A 1990
- (375) Olsen; US 4006403 A 1977
- (376) Olson; US 5364797 A 1994 HCAPLUS
- (377) Oueyssac; US 5089877 A 1991
- (378) Ovshinsky; US 4646266 A 1987
- (379) Ovshinsky; US 5225219 A 1994
- (380) Padwa; J Am Chem Soc 1971, V93(1), P543 HCAPLUS
- (381) Padwa; J Org Chem 1976, V41(1), P180 HCAPLUS
- (382) Padwa; J Org Chem 1976, V41(3), P543 HCAPLUS
- (383) Pasqualini; US 5288476 A 1994 HCAPLUS
- (384) Pasqualini; US 5400278 A 1994 HCAPLUS
- (385) Pasqualini; US 5399339 A 1995 HCAPLUS
- (386) Patek; Tetrahedron Lett 1994, V35, P9169 HCAPLUS
- (387) Patek; Tetrahedron Lett 1995, V36(13), P2227 HCAPLUS
- (388) Patterson; US 4426124 A 1975
- (389) Patton; US 4933185 A 1990 HCAPLUS
- (390) Pavia; Bioorg & Med Chem Lett 1993, V3(3), P387 HCAPLUS

- (381) Pein; IEEE Transactions on Electron Devices 1993, V40(11)
- (382) Pidgeon; US 4927879 A 1990 HCAPLUS
- (383) Pidgeon; US 4931498 A 1990 HCAPLUS
- (384) Pidgeon; Enzyme Microb Technol 1990, V12, P149 HCAPLUS
- (385) Pierce Chemical Co; Catalog & Handbook 1994
- (386) Pirilla; US 5556762 A 1996 HCAPLUS
- (387) Pirrung; US 5143854 A 1993 HCAPLUS
- (388) Pirrung; US 5401783 A 1995 HCAPLUS
- (389) Fiskin; Diagnostic Biosensor Polymers, ACS Symposium Series No 556, Chap 18 1994
- (400) Pokrowsky; Optics Lett 1993, V18(5), P280 HCAPLUS
- (401) Potash; US 5148356 A 1992
- (402) Potash; US 5296722 A 1994
- (403) Powers; US 4701732 A 1987
- (404) Powers; US 4786277 A 1989
- (405) Powers; Biotech & Bioeng 1989, V33, P173 HCAPLUS
- (406) Prabhu; US 5277724 A 1994
- (407) Prabhu; Proc- SPIE-Int Soc Opt Eng (Proc 1992 Intl Symposium on Microelectronics) 1992, V1847, P601 HCAPLUS
- (408) Psaltis; Byte 1992, P179
- (409) Psaltis; Scientific American 1995, P70
- (410) Qiao; Optics Letters, Selected Papers on Holographic Storage V17(19), P1376
- (411) Qiao; Optics Letts, Selected Papers on Holographic Storage 1993, V18(12), P1004 HCAPLUS
- (412) Randolph; J Am Chem Soc 1995, V117, P5712 HCAPLUS
- (413) Rapp; Innovation Feispect Solid Phase Synth Collect Pap, Int Symp, 1st 1990, P205 HCAPLUS
- (414) Rapp; Pept Chem 1992, Proc Jpn Symp, 2nd 1992, P7 HCAPLUS
- (415) Rapp; Pept, Proc Eur Pept Symp, 20th 1989, P199 HCAPLUS
- (416) Rapp; Pept:Chem Biol, Proc Am Pept Symp, 12th 1992, P529 HCAPLUS
- (417) Rava; US 5545531 A 1996 HCAPLUS
- (418) Reusser; US 4180524 A 1979 HCAPLUS
- (419) Rittler; US 4321069 A 1980 HCAPLUS
- (420) Roesner; US 4434579 A 1984
- (421) Roesner; US 4442307 A 1984
- (422) Roesner; US 4596386 A 1986
- (423) Roesner; US 4796074 A 1989
- (424) Roesner; US 5095362 A 1992
- (425) Sabel; US 5114719 A 1992
- (426) Sakakibara; The Use of Hydrogen Fluoride in Peptide Chemistry, Chap 3
- (427) Saulnier; US 4807140 A 1989
- (428) Sawyers; US 5310686 A 1994 HCAPLUS
- (429) Schatz; US 5270170 A 1993 HCAPLUS
- (430) Schatz; US 5238665 A 1994 HCAPLUS
- (431) Schatz; US 5498539 A 1996 HCAPLUS
- (432) Scheckel; US 5349173 A 1994
- (433) Schlossman; US 5130642 A 1992
- (434) Scott; Biotech 1994, V5, P40 HCAPLUS
- (435) Scott; Current Biology 1994, V5, P40 HCAPLUS
- (436) Scott; Science 1990, V249, P886 HCAPLUS
- (437) Sebestyen; Biorg Med Chem Lett 1993, V3, P413 HCAPLUS
- (438) Secker; US 5442940 A 1995
- (439) Senter; Photochem Photobiol 1985, V42(3), P231 HCAPLUS
- (440) Shacham-Diamand; IEEE Electron Device Lett 1989, V10(5), P180
- (441) Shellhammer; US 5319181 A 1994
- (442) Sherwood; Bio/Technology 1992, V10, P1446 HCAPLUS
- (443) Shinnick; US 4889600 A 1989 HCAPLUS
- (444) Sidman; US 4251357 A 1982 HCAPLUS
- (445) Sidman; US 4450150 A 1984 HCAPLUS
- (446) Simon; Proc Natl Acad Sci USA 1992, V89, P9367 HCAPLUS
- (447) Smith; US 5408007 A 1995 HCAPLUS
- (448) Smith; Methods:A Companion to Methods in Enzymology 1992, V4, P73 HCAPLUS

- (449) Southern; J Mol Biol 1975, V98, P503 HCAPLUS
- (450) Souza; US 5358795 A 1994
- (451) Spatola; Chem Biochem Amino Acids, Pept Proteins 1983, V7, P267 HCAPLUS
- (452) Stankovic; Innovation and Perspectives in Solid Phase Synthesis 1993, P391
- (453) Stewart; Solid Phase Peptide Synthesis, 2d Edition 1984, P53 MEDLINE
- (454) Stokke; US 5318343 A 1993
- (455) Sucholeiki; Tetrahedron Lett 1994, V35, P7337 HCAPLUS
- (456) Sugarman; US 5503805 A 1996 HCAPLUS
- (457) Szalki; Peptides: Structure and Function Proceedings of the Eighth American Peptide Symposium 1983, P579 HCAPLUS
- (458) Tam; US 4567230 A 1985 HCAPLUS
- (459) Tanimoto; IEEE Transactions on Electron Devices 1980, VED-27(3), P517 HCAPLUS
- (460) Tate; US 4958452 A 1990
- (461) Tech; US 5388291 A 1994
- (462) Thakoor; US 4876668 A 1989
- (463) Thiele; J Immunassay 1986, V136(3), P1033 HCAPLUS
- (464) Thompson; US 5410155 A 1995 HCAPLUS
- (465) Thorne; US 4154795 A 1979 HCAPLUS
- (466) Tice; US 4539840 A 1985 HCAPLUS
- (467) Tice; US 4442019 A 1983 HCAPLUS
- (468) Tigelaar; US 5300456 A 1994 HCAPLUS
- (469) Toda; US 5359250 A 1994
- (470) Towbin; Proc Natl Acad Sci USA 1979, V76(9), P4350 HCAPLUS
- (471) Toyanaga; The First Annual Conference of The Society for BioMolecular Screening 1995
- (472) Troyk; US 5012236 A 1991
- (473) Tsang; US 5273666 A 1993 HCAPLUS
- (474) Tsao; J Cell Physiol 1982, V110, P219 HCAPLUS
- (475) Tsikris; US 4161355 A 1979 HCAPLUS
- (476) Tuna; US 5248632 A 1993 HCAPLUS
- (477) Tyler; US 5318354 A 1994
- (478) Urbas; US 5250944 A 1993
- (479) Urbas; US 5352962 A 1993
- (480) Urbas; US 5261772 A 1993
- (481) Urbas; US 5420579 A 1995
- (482) Urbas; US 5422636 A 1995
- (483) Usmani; Diagnostic Biosensor Polymers, ACS Symposium Series No 556 1994, Pvii
- (484) Vachon; US 5334304 A 1994
- (485) Vachon; US 5447533 A 1995
- (486) Vedejs; J Org Chem 1984, V49, P573 HCAPLUS
- (487) Velander; US 5308603 A 1994 HCAPLUS
- (488) Vincent; US 4855903 A 1989
- (489) Vo-Dinh; US 5400136 A 1995 HCAPLUS
- (490) Von Gentzow; US 5389534 A 1995 HCAPLUS
- (491) Wang; J Org Chem 1976, V41(20), P3257 HCAPLUS
- (492) Wehrmacher; US 5073703 A 1991
- (493) Weisman; US 5087570 A 1992
- (494) Wells; US 5452311 A 1995
- (495) Wenzel; US 4569981 A 1986 HCAPLUS
- (496) Wild; Japanese Journal of Applied Physics 1987, V26(Supplement 26-4), P237
- (497) Wild; Proc Int Symp on Optical Memory 1987
- (498) Winquist; Biosensors A Practical Approach, Chap 7 1990
- (499) Wang; Chemistry of Protein Conjugation and Cross Linking 1993, V12, P295
- (500) Wood; US 4241537 A 1989
- (501) Wright; Tetrahedron Lett 1993, V34, P3373 HCAPLUS
- (502) Wrinkler; US 5334261 A 1995 HCAPLUS
- (503) Wysocki; Proc Natl Acad Sci USA 1978, V75(6), P2844 HCAPLUS
- (504) Xiang; Science 1995, V268, P1738 HCAPLUS
- (505) Yamamoto; US 5440511 A 1995

- (506) Yamashita; US 5329769 A 1995
 (507) Yamazaki; US 5449441 A 1995 HCAPLUS
 (508) Yen; Makromol Chem 1989, V190, P69 HCAPLUS
 (509) Terbury; US 5134277 A 1992
 (510) Yoshimura; SPIE, Optical Data Storage and Topical Meeting 1999, V1078 HCAPLUS
 (511) Yun; US 5458633 A 1995
 (512) Samora; US 5444816 A 1995 HCAPLUS
 (513) Leppasaari; Z Naturforsch, B: Chem Sci 1993, V48, P1801 HCAPLUS
 (514) Zhang; Fept 1992, Proc Eur Fept Symp, 22nd 1992, P432
 (515) Cuckerman; J Am Chem Soc 1992, V114, P16646
 (516) Cuckerman; J Med Chem 1994, V37, P2678
 (517) Cuckerman; Proc Natl Acad Sci USA 1992, V89, P4505 HCAPLUS

L43 ANSWER 2 OF 16 HCAPLUS COPYRIGHT 2003 ACS

AN 2002:332714 HCAPLUS

DI 136:337373

TI Computer systems and methods for hierarchical cluster analysis of large sets of biological data including highly dense gene array data

IN Fahy, Erin D.

PA USA

SO U.S. Pat. Appl. Publ., 31 pp.

CODEN: USXEXQ

DT Patent

LA English

IC ICM G01N033-48

ICS G01N015-06; G06F007-00

NCL 702019900

CC 9-16 (Biochemical Methods)

Section cross-reference(s): 3

FAN.CUT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 2002051692	A1	20020802	US 1999-307380	19990915
PRAI	US 1999-307380		19990915		

AB A system and corresponding method analyzes biol. data for sets of test subjects such as gene arrays of group test subjects into clusters and order the clusters into a hierarchy based on similarities and differences of biol. data corresponding to the test subjects. A combination of nonhierarchical clustering and hierarchical clustering methods is used to efficiently and effectively perform hierarchical clustering of such biol. data as highly dense gene arrays contg. many thousand test subjects such as genes. First the test subjects are nonhierarchically clustered according to similarities and differences of their biol. data as detd. by distance techniques. Representative values, such as mean values, of the biol. data are detd. for each nonhierarchical cluster of test subjects. These representative values are then used to hierarchically cluster the nonhierarchical clusters. Biol. data for each test subject is displayed in a row of a table. The rows of the table are arranged by the nonhierarchical clustering and further by the hierarchical clustering. Each value of the biol. data is color coded according to its value to display patterns in the hierarchically clustered biol. data.

ST computer system hierarchical cluster analysis biol dense gene array

IT **Mathematical methods**

(Block; computer systems and methods for hierarchical cluster anal. of large sets of biol. data including highly dense gene array data)

IT **Mathematical methods**

(Chebyshev distance; computer systems and methods for hierarchical cluster anal. of large sets of biol. data including highly dense gene array data)

IT **Mathematical methods**

(Chebyshev; computer systems and methods for hierarchical cluster anal. of large sets of biol. data including highly dense gene array data)

- IT **Mathematical methods**
(City-block; computer systems and methods for hierarchical cluster anal. of large sets of biol. data including highly dense gene array data)
- IT **Education**
(Computer-readable instructions; computer systems and methods for hierarchical cluster anal. of large sets of biol. data including highly dense gene array data)
- IT **Mathematical methods**
(Cosine; computer systems and methods for hierarchical cluster anal. of large sets of biol. data including highly dense gene array data)
- IT **Mathematical methods**
(Euclidean distance detns.; computer systems and methods for hierarchical cluster anal. of large sets of biol. data including highly dense gene array data)
- IT **Mathematical methods**
(Euclidean; computer systems and methods for hierarchical cluster anal. of large sets of biol. data including highly dense gene array data)
- IT **Computers**
(Hard drives; computer systems and methods for hierarchical cluster anal. of large sets of biol. data including highly dense gene array data)
- IT **Mathematical methods**
(Isodata; computer systems and methods for hierarchical cluster anal. of large sets of biol. data including highly dense gene array data)
- IT **Mathematical methods**
(Mannhattan distance; computer systems and methods for hierarchical cluster anal. of large sets of biol. data including highly dense gene array data)
- IT **Mathematical methods**
(Minkowski; computer systems and methods for hierarchical cluster anal. of large sets of biol. data including highly dense gene array data)
- IT **Mathematical methods**
(Parallel threshold; computer systems and methods for hierarchical cluster anal. of large sets of biol. data including highly dense gene array data)
- IT **Mathematical methods**
(Pearson correlation; computer systems and methods for hierarchical cluster anal. of large sets of biol. data including highly dense gene array data)
- IT **Mathematical methods**
(Percent disagreement; computer systems and methods for hierarchical cluster anal. of large sets of biol. data including highly dense gene array data)
- IT **Computer program**
(Perl script language; computer systems and methods for hierarchical cluster anal. of large sets of biol. data including highly dense gene array data)
- IT **Mathematical methods**
(Power distance; computer systems and methods for hierarchical cluster anal. of large sets of biol. data including highly dense gene array data)
- IT **Mathematical methods**
(Sequential threshold; computer systems and methods for hierarchical cluster anal. of large sets of biol. data including highly dense gene array data)
- IT **Mathematical methods**
(Squared Euclidean; computer systems and methods for hierarchical cluster anal. of large sets of biol. data including highly dense gene array data)
- IT **Construction materials**
(blocks; computer systems and methods for hierarchical cluster anal. of large sets of biol. data including highly dense gene array data)

- IT Color
(coding; computer systems and methods for hierarchical cluster anal. of large sets of biol. data including highly dense gene array data)
- IT Optical imaging devices
(color, monitors; computer systems and methods for hierarchical cluster anal. of large sets of biol. data including highly dense gene array data)
- IT Agglomeration
Clusters
 - Computer application
 - Computer program
 - Computers
 - Configuration
 - DNA microarray technology
 - Databases
 - Human
 - Information, biological
 - Optical ROM disks
 - Optimization
 - Statistical analysis
(computer systems and methods for hierarchical cluster anal. of large sets of biol. data including highly dense gene array data)
- IT Gene
Proteins
FL: BSU (Biological study, unclassified); BIOL (Biological study)
(computer systems and methods for hierarchical cluster anal. of large sets of biol. data including highly dense gene array data)
- IT Information systems
(data, Biol.; computer systems and methods for hierarchical cluster anal. of large sets of biol. data including highly dense gene array data)
- IT Gene
FL: BSU (Biological study, unclassified); BIOL (Biological study)
(expression; computer systems and methods for hierarchical cluster anal. of large sets of biol. data including highly dense gene array data)
- IT Cluster analysis
(hierarchical; computer systems and methods for hierarchical cluster anal. of large sets of biol. data including highly dense gene array data)
- IT Mathematical methods
(k-means; computer systems and methods for hierarchical cluster anal. of large sets of biol. data including highly dense gene array data)
- IT Computer program
(spreadsheet; computer systems and methods for hierarchical cluster anal. of large sets of biol. data including highly dense gene array data)
- IT Information systems
(storage; computer systems and methods for hierarchical cluster anal. of large sets of biol. data including highly dense gene array data)
- IT Audiovisual aids
(tables; computer systems and methods for hierarchical cluster anal. of large sets of biol. data including highly dense gene array data)

L43 ANSWER 9 OF 16 HCAPLUS COPYRIGHT 2003 ACS

AN 2002:165034 HCAPLUS

DN 136:213153

TI Remotely programmable matrices with memories

IN Nova, Michael P.; Senyei, Andrew E.

PA Discovery Partners International, Inc., USA

SO U.S., 29 pp., Cont.-in-part of U. S. 5,741,462.

CODEN: USXXAM

DT Patent
 LA English
 IC ICM C12M001-34
 ICS C12Q004-68; G01N033-53; C07H021-04; C07EC14-00
 NCL 435287100
 CC 9-1 (Biochemical Methods)
 S- which cross-reference(s): 7, 80
 FAN.CNT 20

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 6052854	B1	20000305	US 1995-430147	19950607
	US 5741462	A	19980421	US 1995-438661	19950425
	US 5874214	A	19990213	US 1995-538387	19951003
	US 6015129	A	20000211	US 1995-567746	19951205
	CA 2216645	AA	19961111	CA 1996-2316645	19960425
	WO 9636436	A1	19961121	WO 1996-036145	19960425
	W: AL, AM, AT, AU, AC, BP, BG, BR, BY, CA, CH, CN, CS, DE, DK, EE,				
	ES, FI, GB, GE, HU, IE, JP, KE, KG, KP, KR, KZ, LK, LR, LS, LT,				
	LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE,				
	SG, SI				
	FW: KE, LS, MW, SD, SE, SG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR,				
	IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN				
EP 222861	A1	19980211	EP 1996-916437	19960425	
	F: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,				
	IE, SI, LT, LV, FI				
CN 1181720	A	19980513	CN 1996-198174	19960425	
JP 11511038	T2	19990916	JP 1996-570562	19960425	
AU 9659185	A1	19961119	AU 1996-59185	19960501	
AU 707444	B2	19990708			
US 6100026	A	20000808	US 1996-637410	19960610	
US 6319668	B1	20011120	US 1996-663752	19960614	
US 6284459	B1	20010904	US 1996-711426	19960905	
US 6017496	A	20000115	US 1996-709435	19960906	
US 5961927	A	19991005	US 1996-723423	19960930	
US 6329139	B1	20011211	US 1997-912996	19970811	
US 6340588	B1	20010122	US 1996-51022	19960922	
PRAI	US 1995-438662	A2	19950425		
	US 1995-184504	A2	19950607		
	US 1995-473660	A	19950607		
	US 1995-430147	A2	19950607		
	US 1995-480196	A	19950607		
	US 1995-484486	A	19950607		
	US 1995-484504	A1	19950607		
	US 1995-538387	A2	19951003		
	US 1995-567746	A	19951205		
	US 1996-629813	A	19960402		
	WO 1996-036145	W	19960425		
	US 1996-633410	A1	19960610		
	US 1996-669252	A2	19960614		
	US 1996-711426	A2	19960905		
	US 1996-709435	A1	19960906		
	US 1996-723423	A2	19960930		
	WO 1996-0315999	A2	19961003		
	US 1996-726703	E2	19961007		
	US 1996-743984	A2	19961023		
	US 1996-741635	E2	19961031		
	US 1997-857800	E2	19970122		
	US 1997-826253	E2	19970327		
	US 1997-945053	E2	19971021		

AB Combinations, called matrixes with memories, of matrix materials with remotely addressable or remotely programmable recording devices that contain at least one data storage unit are provided. The matrix materials are those that are used in as supports in solid phase chem. and biochem.

syntheses, immunoassays and hybridization reactions. The data storage units are preferably nonvolatile antifuse memories. By virtue of this combination, mols. and biol. particles, such as phage and viral particles and cells, that are in proximity or in phys. contact with the matrix combination can be labeled by programming the memory with identifying information and can be identified by retrieving the stored information. Combinations of matrix materials, memories, and linked mols. and biol. materials are also provided. The combinations have a multiplicity of applications, including combinatorial chem., isolation and purifn. of target macromols., capture and detection of macromols. for anal. purposes, selective removal of contaminants, enzymic catalysis, chem. modification and other uses.

ST remotely programmable matrixes memory; memory device program app array
combinatorial phage library
IT Electromagnetic field
(as tags; remotely programmable matrixes with memories)
IT Chromatographs
(columns; remotely programmable matrixes with memories)
IT Containers
(contd. the matrixes with memories; remotely programmable matrixes with memories)
IT **Information systems**
(data; remotely programmable matrixes with memories)
IT Immunoassay
(immunoblotting; remotely programmable matrixes with memories)
IT Analytical apparatus
Antifuses
Combinatorial chemistry
Combinatorial library
Computer application
DNA microarray technology
Immobilization, molecular
Immunoassay
Memory devices
Microtiter plates
Northern blot hybridization
Nucleic acid hybridization
optical detectors
Phage display library
Process automation
Solid phase synthesis
Southern blot hybridization
Test tubes
Vials
(remotely programmable matrixes with memories)

IT DNA
Proteins
ECIA
EL: ANT (Analyte); CRT (Combinatorial reactant); RCT (Reactant); ANST
(Analytical study); CMBI (Combinatorial study); FACT (Reactant or reagent)
(remotely programmable matrixes with memories)
IT 9904-70-0, Nitrocellulose
EL: DEV (Device component use); USES (Uses)
(remotely programmable matrixes with memories)

RE.CNT 62 THERE ARE 62 CITED REFERENCES AVAILABLE FOR THIS RECORD

RE

- (1) Anon; JP 57016359 A 1982
- (2) Anon; GB 2129551 1984
- (3) Anon; FR 2355744 1985
- (4) Anon; EP 0196174 A2 1986 HCAPLUS
- (5) Anon; EP 0419688 A2 1991
- (6) Anon; EP 0578059 B1 1993 HCAPLUS
- (7) Anon; EP 0541349 A2 1993 HCAPLUS

- (8) Anon; EP 0554355 A1 1993 HCAPLUS
- (9) Anon; DE 4419169 A1 1993
- (10) Anon; DE 4313-07 A1 1993
- (11) Anon; DE 4306563 A1 1994 HCAPLUS
- (12) Anon; WO 9413401 1994
- (13) Anon; DE 9416179 U1 1994
- (14) Anon; EP 0640826 A1 1995
- (15) Anon; WO 9711399 1997 HCAPLUS
- (16) Anon; WO 9811036 1998 HCAPLUS
- (17) Anon; WO 9846549 1998 HCAPLUS
- (18) Anon; WO 9846549 1998 HCAPLUS
- (19) Anon; WO 9846550 1998 HCAPLUS
- (20) Bauhahn; US 5483387 A 1996
- (21) Beck-Sickinger; Peptide Research 1991, V4(2), P88 HCAPLUS
- (22) Boigel; US 5214409 A 1993
- (23) Biernat; US 5119099 A 1994
- (24) Brennan; US 5474796 A 1995 HCAPLUS
- (25) Cargill; US 5770455 A 1998 HCAPLUS
- (26) Carroll; US 4857393 A 1989
- (27) Chan; US 5120662 A 1993 HCAPLUS
- (28) Dower; US 5639603 A 1997 HCAPLUS
- (29) Dower; US 5708153 A 1998 HCAPLUS
- (30) Durley; US 5075077 A 1991 HCAPLUS
- (31) Engelhardt; US 3781120 A 1973
- (32) Frank; US 3692495 A 1973 HCAPLUS
- (33) Heller; US 5685662 A 1997 HCAPLUS
- (34) Henshaw; US 5319629 A 1994
- (35) Hudson; US 5545275 A 1996 HCAPLUS
- (36) Isailovic; Videodisc and Optical Memory Systems 1989, P1
- (37) Janda; PNAS 1994, V91, P10779 HCAPLUS
- (38) Janda, K; Proc Natl Acad Sci USA 1994, V91, P10779 HCAPLUS
- (39) Jung; Angew Chem Int Ed Engl 1992, V31(4), P307
- (40) Koreyasu; US 5348705 A 1994
- (41) Mandeck; US 5641634 A 1997 HCAPLUS
- (42) Mioduski; US 3782313 A 1975 HCAPLUS
- (43) Moran; J Am Chem Soc 1995, V117, P10787 HCAPLUS
- (44) Moran; J Am Chem Society 1995, V117, P10787 HCAPLUS
- (45) Nicolaou; Angewandte Chemie 1995, V107(20), P2476
- (46) Nosaka; US 4133642 A 1979
- (47) Nova; US 5741462 A 1998 HCAPLUS
- (48) Nova; US 5751629 A 1998
- (49) Nova; US 5874214 A 1999 HCAPLUS
- (50) Nova; US 5925562 A 1999 HCAPLUS
- (51) Nova; US 5961903 A 1999 HCAPLUS
- (52) Nova; US 6019129 A 2000 HCAPLUS
- (53) Ojima; US 4908813 A 1990
- (54) Foessner; US 5095362 A 1992
- (55) Shah; US 4935875 A 1990
- (56) Still; US 5305334 A 1994 HCAPLUS
- (57) Thakoor; US 4876668 A 1989
- (58) Thorne; US 4154795 A 1979 HCAPLUS
- (59) Tsang; US 5271666 A 1993 HCAPLUS
- (60) Urbas; US 5292362 A 1993
- (61) Vincent; US 4855909 A 1989
- (62) Yaguchi; US 4278787 A 1994

143 ANSWER 10 OF 16 HCAPLUS COPYRIGHT 2003 ACS

AN 2001:916365 HCAPLUS

PN 136:34255

TI Remotely programmable matrices with memories

IN Nova, Michael P.; Senyei, Andrew E.; David, Gary S.

PA Discovery Partners International, USA

SO U.S., 35 pp., Cont.-in-part of U.S. Ser. No. 428,662.

CODEN: USXXAM
 DT Patent
 LA English
 IC ICM G01N015-06
 ICS G01N033-53; C12Q001-68; A61K038-00
 NCL 4220-8100
 CC 9-1 (Biochemical Methods)
 Section cross-reference(s): 7, 80

FAN.CET 20

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 6331273	B1	20011213	US 1995-473660	19950607
	US 6741462	A	19950421	US 1995-423662	19950425
	US 5915562	A	19950720	US 1995-480196	19950607
	US 5874214	A	19990123	US 1995-538387	19951003
	US 6025129	A	20000215	US 1995-567746	19951205
	CA 2216645	AA	19961121	CA 1996-2216645	19960425
	WO 9636436	A1	19961121	WO 1996-US6145	19960425
	W: AL, AM, AT, AU, AC, BR, EG, BR, BY, CA, CH, CN, CS, DE, DK, EE, EC, FI, GB, GE, HU, IC, JP, KE, KG, KP, KR, KZ, LL, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI				
	FW: FE, LS, MW, SD, SE, US, AT, BE, CH, DE, EK, ES, FI, FL, GE, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN				
EP	602861	A1	19960211	EP 1996-616437	19960425
	P: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI				
CN	1181729	A	19980513	CN 1996-193374	19960425
JP	11511238	T2	19990908	JP 1996-530562	19960425
AU	6659185	A1	19961129	AU 1996-59185	19960501
AU	707444	B2	19990708		
US	6100026	A	20000808	US 1996-633410	19960610
US	6319608	B1	20011129	US 1996-669032	19960624
US	6384459	B1	20010904	US 1996-711426	19960905
US	6017496	A	20000125	US 1996-709435	19960906
US	5961923	A	19991005	US 1996-723423	19960930
US	6329139	B1	20011211	US 1997-917998	19970811
US	6340543	B1	20010112	US 1996-51022	19980922
PRAI	US 1995-428662	A2	19950425		
	US 1995-480196	A	19950607		
	US 1995-184504	A2	19950607		
	US 1995-473660	A	19950607		
	US 1995-480147	A2	19950607		
	US 1995-484486	A	19950607		
	US 1995-484504	A2	19950607		
	US 1995-538387	A2	19951003		
	US 1995-567746	A	19951205		
	US 1996-639813	A	19960402		
WO	1996-US6145	W	19960425		
US	1996-633410	A2	19960610		
US	1996-669032	A2	19960624		
US	1996-711426	A1	19960905		
US	1996-709435	A2	19960906		
US	1996-723423	A2	19960930		
WO	1996-US15929	A1	19961003		
US	1996-726703	B2	19961007		
US	1996-743984	A2	19961028		
US	1996-741685	B2	19961031		
US	1997-857800	B2	19970122		
US	1997-816253	B1	19970327		
US	1997-945013	B2	19971021		

AB The invention concerns combinations, called matrixes with memories, of matrix materials with remotely addressable or remotely programmable

recording devices that contain at least one data storage unit are provided. The matrix materials are those that are used in as supports in solid phase chem. and biochem. syntheses, immunoassays and hybridization reactions. The data storage units are preferably non-volatile antifuse memories. By virtue of this combination, mols. and biol. particles, such as phage and viral particles and cells, that are in proximity or in phys. contact with the matrix combination can be labeled by programming the memory with identifying information and can be identified by retrieving the stored information. Combinations of matrix materials, memories, and linked mols. and biol. materials are also provided. The combinations have a multiplicity of applications, including combinatorial chem., isolation and purifn. of target macromols., capture and detection of macromols. for anal. purposes, selective removal of contaminants, enzymic catalysis, chem. modification and other uses. Methods for electronically tagging mols. are biol. particles and matrix support materials and immunoassays and other methods are also provided. Diagrams describing the app. are given.

- ST memory device program app array combinatorial phage library
- IT Electromagnetic field
(as tags; remotely programmable matrixes with memories)
- IT Chromatographs
(columns; remotely programmable matrixes with memories)
- IT Containers
(contg. the matrixes with memories; remotely programmable matrixes with memories)
- IT **Information systems**
(data; remotely programmable matrixes with memories)
- IT Immunoassay
(immunoblotting; remotely programmable matrixes with memories)
- IT Analytical apparatus

Antifuses

Combinatorial chemistry
Combinatorial library

Computer application

DNA microarray technology
Immobilization, molecular
Immunoassay

Memory devices

Microtiter plates
Northern blot hybridization
Nucleic acid hybridization
Optical detectors
Phage display library
Process automation
Solid phase synthesis
Southern blot hybridization
Test tubes
Vials

(remotely programmable matrixes with memories)

- IT DNA

Proteins

RNA

FL: ANT (Analyte); CRT (Combinatorial reactant); ECT (Reactant); ANST
(Analytical study); CMBI (Combinatorial study); EACT (Reactant or reagent)
(remotely programmable matrixes with memories)

- IT 9004-70-0, Nitrocellulose

FL: DEV (Device component use); USES (Uses)

(remotely programmable matrixes with memories)

RE.CNT 503 THERE ARE 503 CITED REFERENCES AVAILABLE FOR THIS RECORD

RE

- (1) Abadeer; US 5334880 1994
- (2) Afeyan; US 5389449 1995 HCAPLUS
- (3) Agrafiotis; US 5463564 1995

(4) Akaogi; US 5452251 1995
(5) Aldwin; US 5491074 1996 HCAPLUS
(6) Andrews; US 5099226 1992
(7) Anon; FR 2110030 HCAPLUS
(8) Anon; FR 2526169
(9) Anon; FR 2555744
(10) Anon; EP 430177 A1
(11) Anon; DE 43130659 A1
(12) Anon; DE 4301401 A1 HCAPLUS
(13) Anon; DE 43065639 A1
(14) Anon; DE 4310169 A1
(15) Anon; DE 4313807 A1
(16) Anon; EP 637750 A2 HCAPLUS
(17) Anon; DE 9416270 A1
(18) Anon; FR 2110030 1972 HCAPLUS
(19) Anon; DE 2344930 1974
(20) Anon; JP 57016359 1981
(21) Anon; FR 2526169 1983
(22) Anon; WO 8401031 1984 HCAPLUS
(23) Anon; FR 2555744 1985
(24) Anon; EP 0136174 1986 HCAPLUS
(25) Anon; WO 8603840 1986 HCAPLUS
(26) Anon; WO 8801302 1988 HCAPLUS
(27) Anon; WO 8901157 1989 HCAPLUS
(28) Anon; WO 8908764 1989
(29) Anon; EP 0378099 1990 HCAPLUS
(30) Anon; WO 9015070 1990 HCAPLUS
(31) Anon; EP 0410688 1991
(32) Anon; EP 0420177 1991
(33) Anon; WO 9201268 1992
(34) Anon; WO 9207093 1992 HCAPLUS
(35) Anon; WO 9209300 1992 HCAPLUS
(36) Anon; WO 9210091 1992 HCAPLUS
(37) Anon; WO 9213271 1992
(38) Anon; EP 0526173 1993
(39) Anon; EP 0535142 1993
(40) Anon; EP 0541340 1993 HCAPLUS
(41) Anon; EP 0554965 1993 HCAPLUS
(42) Anon; EP 0569215 1993
(43) Anon; DE 4313065 1993
(44) Anon; DE 4310169 1993
(45) Anon; DE 4313807 1993
(46) Anon; WO 9306121 1993 HCAPLUS
(47) Anon; DE 9308204 1993
(48) Anon; WO 9308472 1993 HCAPLUS
(49) Anon; DE 4301401 1994 HCAPLUS
(50) Anon; DE 4306563 1994 HCAPLUS
(51) Anon; WO 9402634 1994 HCAPLUS
(52) Anon; WO 9405894 1994 HCAPLUS
(53) Anon; WO 9408051 1994 HCAPLUS
(54) Anon; WO 9411388 1994 HCAPLUS
(55) Anon; WO 9413402 1994
(56) Anon; WO 9413623 1994 HCAPLUS
(57) Anon; WO 9414380 1994 HCAPLUS
(58) Anon; DE 9416270 1994
(59) Anon; WO 9417398 1994 HCAPLUS
(60) Anon; WO 9422889 1994 HCAPLUS
(61) Anon; WO 9426413 1994 HCAPLUS
(62) Anon; WO 9428424 1994 HCAPLUS
(63) Anon; EP 0637750 1995 HCAPLUS
(64) Anon; EP 0640116 1995
(65) Anon; WO 9509550 1995 HCAPLUS
(66) Anon; WO 9502566 1995 HCAPLUS

- (67) Anon; WO 9512008 1995 HCAPLUS
(68) Anon; WO 9519567 1995 HCAPLUS
(69) Anon; WO 9623749 1996 HCAPLUS
(70) Anon; WO 9624061 1996 HCAPLUS
(71) Anon; GB 2306408 1997
(72) Anon; GB 2306484 1997 HCAPLUS
(73) Anon; WO 9714941 1997 HCAPLUS
(74) Anon; WO 9719953 1997 HCAPLUS
(75) Anon; WO 9720073 1997 HCAPLUS
(76) Anon; WO 9720074 1997 HCAPLUS
(77) Anon; Angew Chem 1995, V107(20), P2476
(78) Anon; Biochem 1972, V11(5), P942
(79) Anon; NASAT50H 1996
(80) Anon; Pierce Chemical Co Catalog & Handbook 1994
(81) Anon; Scrip 1995, P11
(82) Anon; <http://www.ircori.com/products.html> 1996
(83) Arenzen; US 5342772 1994 HCAPLUS
(84) Ayers; US 4175183 1979 HCAPLUS
(85) Ayers; US 4178439 1979 HCAPLUS
(86) Bakalash; US 5361385 1994
(87) Baldwin; J Am Chem Soc 1995, V117, P5588 HCAPLUS
(88) Balint; US 4691870 1987 HCAPLUS
(89) Barany; Int J Peptide Protein Res 1987, V30, I705 HCAPLUS
(90) Barrett; US 5252743 1993 HCAPLUS
(91) Barrett; US 5451683 1995 HCAPLUS
(92) Barrett; US 5482867 1996 HCAPLUS
(93) Basch; J Immunol Meths 1983, V56, P269 MEDLINE
(94) Batra; Molecular Immunol 1993, V30(4), P379 HCAPLUS
(95) Baum; C&EN 1994, P30
(96) Bayer; US 4904405 1990 HCAPLUS
(97) Bayer; US 5222314 1994 HCAPLUS
(98) Bayer; Chem Pept Proteins 1986, V3, P3 HCAPLUS
(99) Bayer; Pept;Chem, Struct Biol, Proc Am Pept Symp, 13th 1994, P156 HCAPLUS
(100) Bayer; Pept;Struct Funct Proc Am Pept Symp, 8th 1983, P87 HCAPLUS
(101) Bayer; Poly-(Ethylene Glycol) Chem 1992, P325 HCAPLUS
(102) Beck-Sickinger; Peptide Research 1991, V4(2), P83 HCAPLUS
(103) Beigel; US 4333072 1981
(104) Beigel; US 5214409 1993
(105) Beigel; US 5235526 1993
(106) Beigel; US 5237911 1993
(107) Beigel; US 5266926 1993
(108) Bell; US 5435937 1995 HCAPLUS
(109) Berg; Innovation Perspect Solid Phase Synth Collect Pap, Int Symp, 1st 1990, P453 HCAPLUS
(110) Berg; J Am Chem Soc 1969, V111, P8024 HCAPLUS
(111) Berg; Pept, Proc Eur Pept Symp P196
(112) Piebricher; US 4177038 1979 HCAPLUS
(113) Biernat; US 3119999 1964
(114) Birz; US 3704952 1972 HCAPLUS
(115) Birge; US 5228061 1993
(116) Birge; US 5253198 1993
(117) Birge; Ann Rev Phys Chem 1990, V41, P633 HCAPLUS
(118) Bloom; Electronics Systems Design Magazine 1989, P5
(119) Boardman; US 5290734 1994 HCAPLUS
(120) Boldt; J Immunol 1979, V123(2), P808 HCAPLUS
(121) Borman; Chem & Engin News 1990, P29
(122) Braatz; US 5403750 1995 HCAPLUS
(123) Bradley; US 5130572 1992
(124) Brandt; High-throughput screening:An overview 1995, P21 MEDLINE
(125) Brenner; Proc Natl Acad Sci USA 1992, V89, P5381 HCAPLUS
(126) Brigham-Burke; US 5395587 1995 HCAPLUS
(127) Brizzolara; US 5246355 1993
(128) Brizzolara; US 5366733 1994 HCAPLUS

- (129) Brown; US 5116422 1994 HCAPLUS
(130) Brown; Oligonucleotides Analogues 1991, P1
(131) Buechler; US 5089391 1992 HCAPLUS
(132) Buechler; Clin Chem 1992, V35(9), P1678 HCAPLUS
(133) Bunin; J Am Chem Soc 1994, V114, P10997 HCAPLUS
(134) Bunin; Proc Natl Acad Sci USA 1994, V91, P4708 HCAPLUS
(135) Burgess; J Med Chem 1994, V37, P2385 HCAPLUS
(136) Butcher; US 4991719 1991
(137) Butz; Peptide Res 1994, V7(1), P20 HCAPLUS
(138) Campbell; US 5002148 1991
(139) Campbell; US 5014727 1991
(140) Campbell; US 5074313 1991
(141) Campbell; US 5359115 1994 HCAPLUS
(142) Campbell; US 5362899 1994 HCAPLUS
(143) Campbell; US 5420326 1995 HCAPLUS
(144) Campbell; US 5434336 1995
(145) Campbell; J Am Chem Soc 1995, V117, P5381 HCAPLUS
(146) Cargill; US 5609876 1997 HCAPLUS
(147) Carroll; US 4857893 1989
(148) Carroll; US 4952438 1990
(149) Carroll; US 5347363 1994
(150) Chan; US 5110661 1992 HCAPLUS
(151) Chang; US 5326696 1994 HCAPLUS
(152) Chen; US 5381035 1995 HCAPLUS
(153) Chen; J Am Chem Soc 1994, V116, P2661 HCAPLUS
(154) Cherukuri; US 4952531 1990 HCAPLUS
(155) Cherukuri; US 5043221 1991 HCAPLUS
(156) Cherukuri; US 5047371 1991 HCAPLUS
(157) Cherukuri; US 5256469 1993
(158) Chiang; US 5316971 1994 HCAPLUS
(159) Clarkson; Nature 1991, V352, P624 HCAPLUS
(160) Cody; US 5324483 1994 HCAPLUS
(161) Cohen; US 5270251 1993
(162) Cohen; IEEE Transactions on Electron Devices 1994, V41(5), P721
(163) Coles; US 5314825 1994 HCAPLUS
(164) Cook; Proc IEEE Popular Circuits Technol Meet 1986, P99
(165) Coupek; US 4171411 1979 HCAPLUS
(166) Cozzette; US 5200051 1993 HCAPLUS
(167) Crane; US 5092992 1992 HCAPLUS
(168) Cunningham; US 5326449 1994 HCAPLUS
(169) Cwirla; Proc Natl Acad Sci USA 1990, V87, P6378 HCAPLUS
(170) Czarnik; Polym Prepr (Am Chem Soc, Div Polym Chem) 1994, V35(2), P985 HCAPLUS
(171) D'Hont; US 5351051 1994
(172) Dandekar; US 4777019 1988
(173) Darrow; US 5255650 1993
(174) Darrow; US 5265610 1993
(175) Dattagupta; US 4941193 1985 HCAPLUS
(176) Dattagupta; US 5115849 1993 HCAPLUS
(177) Dave; Anal Chem 1994, V66(22), P1120A HCAPLUS
(178) David; US 4376110 1983 HCAPLUS
(179) Davis; US 5258289 1993 HCAPLUS
(180) de Witt; Proc Natl Acad Sci USA 1993, V90, P6909 HCAPLUS
(181) Desai; US 5334649 1994 HCAPLUS
(182) Desai; US 5416191 1995 HCAPLUS
(183) Devlin; Science 1990, V249, P404 HCAPLUS
(184) Dewitt; Drug Develop Res 1994, V33, P116 HCAPLUS
(185) Dewitt; Proc Natl Acad Sci USA 1993, V90, P6909 HCAPLUS
(186) Dillon; US 5395750 1995 HCAPLUS
(187) Ditz; US 5121746 1992 HCAPLUS
(188) Dixit; US 5323812 1994 HCAPLUS
(189) Dixit; US 5329137 1994 HCAPLUS
(190) Domkowski; US 4682528 1987

- (191) Dorman; US 4795803 1997
- (192) Dorman; Biochemistry 1994, V33(19), P5661 HCAPLUS
- (193) Dower; US 5432013 1995 HCAPLUS
- (194) Dower; US 5547539 1996 HCAPLUS
- (195) Dower; Annu Rep Med Chem 1991, V26, P271 HCAPLUS
- (196) Dwyer; US 4975647 1990
- (197) Dulac; Cell 1994, V83, P195 HCAPLUS
- (198) Dumoulin; US 5211165 1993
- (199) Dumoulin; US 5251635 1993
- (200) Dumoulin; US 5271400 1993
- (201) Dumoulin; US 5307808 1994
- (202) Dumoulin; US 5377678 1995
- (203) Dumoulin; US 5437277 1995
- (204) Dumoulin; US 5443066 1995
- (205) Dumoulin; US 5445150 1995
- (206) Dunlap; Immobilized Biochemicals and Affinity Chromatography, Symposium on Affinity Chromatography and Immobilized Biochemicals 1974
- (207) Dunlap, R; Immobilized Biochemicals and Affinity Chromatography, Part I 1974
- (208) Ecker; Biotechnology 1995, V13, P351 HCAPLUS
- (209) Eichler; Biochem 1993, V12, P11035 HCAPLUS
- (210) Eimori; US 5442312 1995
- (211) Elkins; J Clin Immun 1990, V13(4), P169
- (212) Elkins; US 4745071 1988 HCAPLUS
- (213) Elkins; US 5171093 1992 HCAPLUS
- (214) Elkins; US 5304498 1994 HCAPLUS
- (215) Ellman; US 5288514 1994 HCAPLUS
- (216) Engelhardt; US 3781128 1973
- (217) Eveleigh; US 4885358 1989 HCAPLUS
- (218) Eveleigh; US 4954444 1990 HCAPLUS
- (219) Farah; US 5217743 1993 HCAPLUS
- (220) Fishman; US 3843443 1974 HCAPLUS
- (221) Fodor; US 5324633 1994
- (222) Fodor; US 5424186 1995 HCAPLUS
- (223) Fodor; US 5489678 1996 HCAPLUS
- (224) Fodor; US 5541061 1996 HCAPLUS
- (225) Fodor; Science 1991, V251, P767 HCAPLUS
- (226) Fox; US 4485227 1984 HCAPLUS
- (227) Fraczek; US 5323704 1994
- (228) Frank; US 3692498 1972 HCAPLUS
- (229) Freshney; Culture of Animal Cells A Manual of Basic Technique 1983, P141
- (230) Francke; US 5004600 1991 HCAPLUS
- (231) Furka; Int J Pept Protein Res 1991, V37, P487 HCAPLUS
- (232) Gallop; J Med Chem 1994, V37(9), P1233 HCAPLUS
- (233) Gardosi; US 4654512 1987
- (234) Georger; US 5324591 1994 HCAPLUS
- (235) Georgiou; US 5348867 1994 HCAPLUS
- (236) Geysen; J Immunol Meth 1987, V102, P259 HCAPLUS
- (237) Giampapa; US 5201728 1993 HCAPLUS
- (238) Giese; US 4281287 1981 HCAPLUS
- (239) Giles; US 5028918 1991
- (240) Gilnam; Immobilized Polynucleotides and Nucleic Acids P173
- (241) Gnadinger; US 5273037 1993 HCAPLUS
- (242) Goeddel; US 5213408 1993 HCAPLUS
- (243) Goldmacher; Bioconjugate Chem 1992, V3, P104 HCAPLUS
- (244) Goldsmith; US 5300466 1994 HCAPLUS
- (245) Gordon; US 5397939 1995
- (246) Gordon; J Med Chem 1994, V37(10), P1385 HCAPLUS
- (247) Gould; US 4434585 1984 HCAPLUS
- (248) Gray; US 5288613 1994 HCAPLUS
- (249) Grecksch; US 5033623 1991
- (250) Greve; IEEE Transactions on Electron Devices 1982, VED-29(4), P719 HCAPLUS

- (251) Gu; J Optical Soc Am, Selected Papers on Holographic Storage 1992, V9(11), P1978
- (252) Gu; Optics Communications, Selected Papers on Holographic Storage 1992, V93, P113
- (253) Guire; US 4972493 1990 HCAPLUS
- (254) Gustafson; US 5572410 1996
- (255) Gustin; US 5056056 1991
- (256) Haarer; Proc Int Symp on Optical Memory, Japanese Journal of Applied Physics 1987, V26(Supplement 26-4), P217
- (257) Hale; Analytical Biochem 1995, V231, P46 HCAPLUS
- (258) Hammond; US 5374718 1994 HCAPLUS
- (259) Hansen; US 5443953 1995 HCAPLUS
- (260) Harlow; Antibodies A Laboratory Manual, Chap 14 1983
- (261) Hazum; Pept, Proc Eur Pept Symp, 16th 1981, P105 HCAPLUS
- (262) Hendrick; US 5055659 1991
- (263) Hermanson; Chaps 1 and 2, Immobilized Affinity Ligand Techniques 1992
- (264) Hesser; US 4568880 1986
- (265) Hession; US 5117870 1993 HCAPLUS
- (266) Hidaka; US 4908694 1990
- (267) Hilferink; US 5148404 1992
- (268) Hoeman; US 4990756 1991
- (269) Hoey; US 5383873 1995 HCAPLUS
- (270) Hogan; US 5216143 1993 HCAPLUS
- (271) Hollander; US 5029214 1991
- (272) Holmes; US 5143974 1993 HCAPLUS
- (273) Holmes; US 5527681 1996 HCAPLUS
- (274) Holmes; US 5549974 1996 HCAPLUS
- (275) Holzworth; US 5384481 1995
- (276) Hong; Optical Engineering 1995, V34(+), P2193
- (277) Hopfield; US 5063417 1991 HCAPLUS
- (278) Houghton; US 4631211 1986 HCAPLUS
- (279) Houghton; BioTechniques 1993, V13(3), P412 HCAPLUS
- (280) Houghton; Nature 1991, V354, P84 HCAPLUS
- (281) Houghton; Proc Natl Acad Sci USA 1985, V82, P5131 HCAPLUS
- (282) Howard, H; Immobilized Enzyme, Antigens, Antibodies and Peptides Preparation and Characterization 1975
- (283) Hutchinson; US 5218189 1993
- (284) Ilg; Macromolecules 1994, P1778 HCAPLUS
- (285) Ill; Biophys J 1993, V64, P919 HCAPLUS
- (286) Inoue; US 4960983 1990
- (287) Isailovic; Videodisc and Optical Memory Systems 1985, Fiii
- (288) Ishigaki; US 4783776 1988
- (289) Ishihara; US 5119163 1992
- (290) Ishikawa; J Immunoassay 1983, V4(3), P209 HCAPLUS
- (291) Ito; US 5384038 1995 HCAPLUS
- (292) Ito; Polymeric Materials for Microelectronic Applications: Science and Technology, ACS Symposium Series No 579, Chaps 17, 23, 27-29, 35 and 36 1995
- (293) Jakoby, W; Affinity Techniques Enzyme Purification: Part B Methods in Enzymology 1974, V34
- (294) Janda; Proc Natl Acad Sci USA 1994, V91, P10779 HCAPLUS
- (295) Jeong; US 5442584 1995
- (296) Johansson; Methods in Enzymology 1976, V44, P659 HCAPLUS
- (297) Jones; US 5211315 1993 HCAPLUS
- (298) Jung; Angew Chem Int Ed Engl 1992, V31(4), P367
- (299) Jurisch; US 5308967 1994
- (300) Jurisch; Identifikation: kontaktlos via Hochfrequenz, Elektronik 1993, V9, P36
- (301) Kabat; Experimental Immunochemistry, Chapter 40 Equilibrium Dialysis, 1961, P715
- (302) Kacian; US 5336024 1995 HCAPLUS
- (303) Raji; "Molecular Design of Epoxy Resins for Microelectronics Packaging," Chap 17 1994

- (304) Katsube; US 5296122 1994 HCAPLUS
(305) Kaufer; US 4702931 1988 HCAPLUS
(306) Kennedy; Solid Phase Biochemistry, Analytical and Synthetic Aspects 1983, V7, P.53
(307) Kent; Isr J Chem 1978, V17, P243 HCAPLUS
(308) Kessler; Angew Chem Int Ed Engl 1993, V32(4), P543
(309) Kettner; Proc Nat Acad Sci USA 1976, V73(4), P1102 HCAPLUS
(310) Khrapko; FEBS Lett 1989, V256, P118 HCAPLUS
(311) Kick; J Med Chem 1995, V38, P1427 HCAPLUS
(312) Kim; US 4179482 1979 HCAPLUS
(313) Kimura; US 5311030 1994 HCAPLUS
(314) King; US 5401371 1995 HCAPLUS
(315) Kip; US 5195190 1993
(316) Kleine; Immunobiol 1994, V190, P53 HCAPLUS
(317) Kleinman; Analytical Biochem 1987, V166, P1 HCAPLUS
(318) Koert; US 5410486 1995
(319) Koreyasu; US 5348705 1994
(320) Krizek; US 5347283 1994
(321) Kwoh; Proc Natl Acad Sci USA 1989, V86, P1173 HCAPLUS
(322) Ladner; US 5223409 1993 HCAPLUS
(323) Ladner; US 5260203 1993 HCAPLUS
(324) Lake; US 5350645 1994
(325) Lam; US 5382513 1995 HCAPLUS
(326) Lam; Nature 1984, P82 HCAPLUS
(327) Landt; US 5030807 1991
(328) Langer; US 4657543 1987 HCAPLUS
(329) Langer; US 4779806 1988
(330) Le; US 5064767 1991 HCAPLUS
(331) Lee; US 5250459 1993 HCAPLUS
(332) Lee; US 5281158 1994
(333) Lehn; US 5457184 1995 HCAPLUS
(334) Levin; US 5100626 1992
(335) Lewis; US 5346789 1994
(336) Li; Applied Optics 1994, V33(17), P3764
(337) Ligler; US 5391463 1995 HCAPLUS
(338) Limisimaque; US 4870574 1989
(339) Ling; US 3367517 1975 HCAPLUS
(340) Liskamp; Angew Chem Int Ed Engl 1994, V33(6), P633
(341) Loetscher; J Chromatography 1992, V595, P113 HCAPLUS
(342) Loetscher; J Chromatography 1992, V595, P113 HCAPLUS
(343) Lowe; US 4562157 1985 HCAPLUS
(344) Maerli; Reactive Polymers 1994, V10, P203 HCAPLUS
(345) Mage; Eur J Immunol 1981, V11, P238 MEDLINE
(346) Mage; J Immunol Methods 1977, V15, P47 MEDLINE
(347) Magel; US 5412593 1995
(348) Manddecki; US 5641634 1997 HCAPLUS
(349) Martin; J Med Chem 1995, V38, P1431 HCAPLUS
(350) Matthews; US 3999123 1976 HCAPLUS
(351) Maucclair; US 5283371 1993 HCAPLUS
(352) McIntyre; US 4318658 1982
(353) McKeehan; J Cell Biol 1976, V71, P727 HCAPLUS
(354) Merrifield; US 4006117 1977 HCAPLUS
(355) Merrifield; Biochemistry 1964, V3(9), P1385 HCAPLUS
(356) Mier; US 5211050 1993 HCAPLUS
(357) Miles; Nature 1966, V212, P186 HCAPLUS
(358) Milliman; US 5330831 1995 HCAPLUS
(359) Milliman; US 5384747 1994 HCAPLUS
(360) Milliman; US 5291874 1994 HCAPLUS
(361) Milliman; US 5352579 1994 HCAPLUS
(362) Mitchell; J Org Chem 1979, V43(14), P2845 HCAPLUS
(363) Mitchell; J Org Chem 1978, V43(14), P2845 HCAPLUS
(364) Mitchell; Tetrahedron Lett 1976, V42, P3795
(365) Mjalli; NetSci 1995, V1(1) HCAPLUS

- (366) Mok; US 5438422 1995
(367) Mok; Optics Lett 1993, V18(11), P915 HCAPLUS
(368) Moran; 31st Annual American Chemical Society Western Regional Meeting & 4th Annual San Diego Biotech Exposition 1995, V117 HCAPLUS
(369) Moran; J Am Chem Soc 1995, V117, P10787 HCAPLUS
(370) Mori; US 5451895 1995
(371) Mullis; US 4683003 1987 HCAPLUS
(372) Munz; US 5044613 1991
(373) Nicolaou; Angew Chem 1995, V107, P2289 HCAPLUS
(374) Nicolaiev; Peptide Research 1992
(375) McGrady; Medicinal Chemistry: A Biochemical Approach 1995, P388
(376) Nishihara; Shimadzu Hyoron 1993, V50, P35 HCAPLUS
(377) Nisaka; US 4133641 1979
(378) Ohmi; US 4791385 1988
(379) Ogima; US 4908813 1990
(380) Olsen; US 4006403 1977
(381) Olson; US 5364797 1994 HCAPLUS
(382) Ovshinsky; US 4646266 1987
(383) Ovshinsky; US 5335219 1994
(384) Padwa; J Am Chem Soc 1971, V93(2), P548 HCAPLUS
(385) Padwa; J Org Chem 1976, V41(1), P139 HCAPLUS
(386) Padwa; J Org Chem 1976, V41(3), P543 HCAPLUS
(387) Pasqualin; US 5300278 1994 HCAPLUS
(388) Pasqualini; US 5384476 1994 HCAPLUS
(389) Pasqualini; US 5393339 1995 HCAPLUS
(390) Patek; Tetrahedron Lett 1994, V35, P9169 HCAPLUS
(391) Patek; Tetrahedron Lett 1995, V36(13), P2227 HCAPLUS
(392) Patterson; US 3920124 1975
(393) Patton; US 4933285 1990 HCAPLUS
(394) Pavia; Bioorg & Med Chem Lett 1993, V3(3), P387 HCAPLUS
(395) Peim; IEEE Transactions on Electron Devices 1993, V40(11)
(396) Pidgeon; US 4927873 1990 HCAPLUS
(397) Pidgeon; US 4931498 1990 HCAPLUS
(398) Pidgeon; Enzyme Microb Technol 1990, V12, P149 HCAPLUS
(399) Pinilla; US 5556762 1996 HCAPLUS
(400) Pirrung; US 5143854 1992 HCAPLUS
(401) Pirrung; US 5495783 1995 HCAPLUS
(402) Pliskin; Diagnostic Biosensor Polymers, ACS Symposium Series No 556, Chap 18 1994
(403) Pokrowsky; Optics Lett 1983, V8(5), P280 HCAPLUS
(404) Potash; US 5148256 1992
(405) Potash; US 5296722 1994
(406) Powers; US 4702732 1987
(407) Powers; US 4786277 1983
(408) Powers; Biotech & Bioeng 1989, V33, P173 HCAPLUS
(409) Prabhu; US 5277724 1994
(410) Prabhu; Proc SPIE-Int Soc Opt Eng (Proc 1990 Intl Symposium on Microelectronics) 1991, V1847, P601 HCAPLUS
(411) Psaltis; Byte 1991, P179
(412) Psaltis; Scientific American 1995, P70
(413) Qiao; Optics Lett, Selected Papers on Holographic Storage 1992, V17(19), P1376
(414) Qiao; Optics Lett, Selected Papers on Holographic Storage 1993, V18(12), P1004 HCAPLUS
(415) Queyssac; US 5089877 1992
(416) Randolph; J Am Chem Soc 1995, V117, P5712 HCAPLUS
(417) Fapp; Innovation Perspect Solid Phase Synth Collect Pap, Int Symp, 1st 1990, P205 HCAPLUS
(418) Fapp; Pept Chem 1992, Proc Jpn Symp, 2nd 1992, P7 HCAPLUS
(419) Fapp; Pept, Proc Eur Pept Symp, 10th 1989, P199 HCAPLUS
(420) Fapp; Pept:Chem Biol, Proc Am Pept Symp, 12th 1992, P529 HCAPLUS
(421) Rava; US 5545531 1996 HCAPLUS
(422) Reusser; US 4139524 1979 HCAPLUS

- (423) Pitter; US 4321069 1982 HCAPLUS
 (424) Poesner; US 4424579 1984
 (425) Poesner; US 4442507 1984
 (426) Poesner; US 4508186 1986
 (427) Poesner; US 4796074 1989
 (428) Poesner; US 5095360 1992
 (429) Poesner; US 5583819 1996
 (430) Sabel; US 5114719 1992
 (431) Sakakibara; The Use of Hydrogen Fluoride in Peptide Chemistry, Chap 3
 (432) Saelnier; US 4807140 1989
 (433) Sawyers; US 5310656 1994 HCAPLUS
 (434) Schatz; US 5270170 1993 HCAPLUS
 (435) Schatz; US 5338665 1994 HCAPLUS
 (436) Schatz; US 5498580 1996 HCAPLUS
 (437) Scheckel; US 5349173 1994
 (438) Schlossman; US 5120642 1992
 (439) Scott; Biotech 1994, V6, P40 HCAPLUS
 (440) Scott; Current Biology 1994, V5, P40 HCAPLUS
 (441) Scott; Science 1990, V243, P386 HCAPLUS
 (442) Sebestyen; Bioorg Med Chem Lett 1993, V3, P413 HCAPLUS
 (443) Secker; US 5442949 1995
 (444) Senter; Photochem Photobiol 1985, V42(3), P331 HCAPLUS
 (445) Service; Science 1995, V270, P577
 (446) Shacham-Diamand; IEEE Electron Device Lett 1989, V10(5), P180
 (447) Shellhammer; US 5319181 1994
 (448) Sherwood; Bio/Technology 1992, V10, P1446 HCAPLUS
 (449) Shinnick; US 4859300 1989 HCAPLUS
 (450) Sidman; US 4351337 1982 HCAPLUS
 (451) Sidman; US 4450150 1984 HCAPLUS
 (452) Simon; Proc Natl Acad Sci USA 1992, V89, P9307 HCAPLUS
 (453) Smith; US 5403037 1995 HCAPLUS
 (454) Smith; Methods: A Comparison to Methods in Enzymology 1992, V4, P73 HCAPLUS
 (455) Southern; J Mol Biol 1975, V83, P503 HCAPLUS
 (456) Souza; US 5353795 1994
 (457) Spatola; Chem Biochem Amino Acids, Pept Proteins 1983, V7, P267 HCAPLUS
 (458) Stankovic; Innovation and Perspectives in Solid Phase Synthesis 1993, P391
 (459) Stewart; Solid Phase Peptide Synthesis, 2d Edition 1984, P53 MEDLINE
 (460) Still; US 5565324 1996 HCAPLUS
 (461) Stokke; US 5218343 1993
 (462) Sucholeiki; Tetrahedron Letts 1994, V35, P7307 HCAPLUS
 (463) Sugarman; US 5503805 1996 HCAPLUS
 (464) Szelke; Peptides: Structure and Function Proceedings of the Eighth American Peptide Symposium 1983, P579 HCAPLUS
 (465) Tam; US 4507230 1985 HCAPLUS
 (466) Tanimoto; IEEE Transactions on Electron Devices 1980, VED-27(3), P517 HCAPLUS
 (467) Tate; US 4958451 1990
 (468) Tech; US 5288291 1994
 (469) Thakoor; US 4876068 1989
 (470) Thiele; J Immunoassay 1986, V13(3), P1038 HCAPLUS
 (471) Thomson; US 5410155 1995 HCAPLUS
 (472) Thorne; US 4154795 1979 HCAPLUS
 (473) Tide; US 4530840 1985 HCAPLUS
 (474) Tide; US 4542025 1985 HCAPLUS
 (475) Tigelaar; US 5300456 1994 HCAPLUS
 (476) Tola; US 5359159 1994
 (477) Towbin; Proc Natl Acad Sci USA 1979, V76(9), P4350 HCAPLUS
 (478) Tovaraga; Abstract presented Tues, the First Annual Conference of the Society for BioMolecular Screening 1995
 (479) Troyk; US 5013236 1991
 (480) Tsang; US 5272666 1994 HCAPLUS
 (481) Tsao; J Cell Physiol 1982, V110, P219 HCAPLUS

- (482) Tsibris; US 4162355 1979 HCAPLUS
 (483) Tung; US 5243621 1993 HCAPLUS
 (484) Tyler; US 5318354 1994
 (485) Urbas; US 5250944 1993
 (486) Urbas; US 5252962 1993
 (487) Urbas; US 5262771 1993
 (488) Urbas; US 5420579 1995
 (489) Urbas; US 5421636 1995
 (490) Usmani; Diagnostic Biosensor Polymers, ACS Symposium Series No 556 1994,
 Pvi1
 (491) Vachon; US 5214334 1994
 (492) Vachon; US 5447533 1995
 (493) Vedejs; J Org Chem 1984, V49, P573 HCAPLUS
 (494) Velander; US 5328603 1994 HCAPLUS
 (495) Vincent; US 4855909 1989
 (496) Vo-Dinh; US 5400136 1995 HCAPLUS
 (497) Von Gentzow; US 5384534 1995 HCAPLUS
 (498) Wang; J Org Chem 1976, V41(L0), P3253 HCAPLUS
 (499) Wehrmacher; US 5073703 1991
 (500) Weissman; US 5087570 1992
 (501) Wells; US 5453311 1995
 (502) Wenzel; US 4569961 1986 HCAPLUS
 (503) Wild; Proc Int Symp on Optical Memory, Japanese Journal of Applied
 Physics 1987, V26(Supplement 16-4), P233
 (504) Winquist; Biosensors A Practical Approach, Chap 7 1990
 (505) Wong; Chemistry of Protein Conjugation and Cross Linking 1993, V12, P295
 (506) Wood; US 4241537 1980
 (507) Wright; Tetrahedron Lett 1993, V34, P3373 HCAPLUS
 (508) Wrinkler; US 5384261 1995 HCAPLUS
 (509) Wysocki; Proc Natl Acad Sci USA 1978, V75(6), P2844 HCAPLUS
 (510) Xiang; Science 1995, V268, P1738 HCAPLUS
 (511) Yamamoto; US 5440511 1995
 (512) Yamashita; US 5389769 1995
 (513) Yamazaki; US 5449941 1995 HCAPLUS
 (514) Yen; Makromol Chem 1989, V190, P69 HCAPLUS
 (515) Yerbury; US 5134277 1993
 (516) Yoshimura; Optical Data Storage Topical Meeting 1989, V1078 HCAPLUS
 (517) Yun; US 5453633 1995
 (518) Zamora; US 5443816 1995 HCAPLUS
 (519) Zeppezauer; Z Naturforsch, B: Chem Sci 1993, V48, P1801 HCAPLUS
 (520) Chang; Pept 1992, Proc Eur Pept Symp, 22nd 1993, P432
 (521) Zuckerman; J Am Chem Soc 1992, V114, P10646
 (522) Zuckerman; J Med Chem 1994, V37, P2678
 (523) Zuckermann; Proc Natl Acad Sci USA 1992, V89, P4505 HCAPLUS

L43 ANSWER 11 OF 16 HCAPLUS COPYRIGHT 2003 ACS

AN 2001:397174 HCAPLUS

DI 154:363648

TI Method, apparatus, media and **signals** for identifying associated
 cell **signaling proteins**

IN **Pelech, Steven**

PA The University of British Columbia, Can.

SO PCT Int. Appl., 90 pp.

CODEN: PIXMDJ

DT **Patent**

LA English

IC ICM 601N973-68

CC **9-1 (Biochemical Methods)**

FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2001033674	A2	20010531	WO 2000-CA1378	20001117
	W: AU, CA, JP, NZ, US				

PW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL,
PT, SE, TR
EP 1134187 A2 20020628 EP 2000-979297 20001117
E: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
IE, FI, CY, TR
PRAI CA 1999-2290335 A 19991119
CA 1999-2290204 A 19991122
US 2000-216357P P 20000705
WO 2000-CA1378 W 20001117
AB Methods, app., media and **signals** for identifying assocd. cell
signaling proteins are disclosed. The method involves
producing and storing a comparison value for each pair of the cell
signaling proteins in response to data values
representing phys. properties of resp. cell **signaling**
proteins. The method further involves identifying cell
signaling protein pairs having comparison values
satisfying a condition indicative of an assocn. between the cell
signaling proteins.
ST app media **signal** identifying cell **signaling**
protein
IT **Memory devices**
(RAM (random access); method, app., media
and **signals** for identifying assocd. cell **signaling**
proteins)
IT **Information systems**
(data; method, app., media and **signals** for
identifying assocd. cell **signaling proteins**)
IT Gene
(expression, co-; method, app., media and **signals** for
identifying assocd. cell **signaling proteins**)
IT Apparatus
Cell
Gel electrophoresis
Memory devices
Physical properties
Polyacrylamide gel electrophoresis
Signal transduction, biological
(method, app., media and **signals** for identifying assocd. cell
signaling proteins)
IT Phosphorylation, biological
(**protein**; method, app., media and **signals** for
identifying assocd. cell **signaling proteins**)
IT **Proteins, specific or class**
FL: ANT (Analyte); ANST (Analytical study)
(**signaling, see**; method, app., media and **signals**
for identifying assocd. cell **signaling proteins**)
IT **Information systems**
(**storage**; method, app., media and **signals** for
identifying assocd. cell **signaling proteins**)
L43 ANSWER 12 OF 16 HCAPLUS COPYRIGHT 2003 ACS
AN 2001:397172 HCAPLUS
DN 139:2565
TI Multiblot kinase analysis
IN **Pelech, Steven**
PA The University of British Columbia, Can.
SO ECT Int. Appl., 61 pp.
CODEN: PIXXD2
DT **Patent**
LA English
IC ICM G01N033-573
CC 9-16 (Biochemical Methods)
Section cross-reference(s): 7

FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2001038877	A2	20010531	WO 2000-CA1377	20001117
	W: AU, CA, JP, NZ, US				
	FW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GE, GR, IE, IT, LU, MC, NL, PT, SE, TR				
	EP 1234184	A2	20020328	EP 2000-973296	20001117
	F: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI, CY, TR				
PRAI	CA 1999-2290335	A	19991119		
	CA 1999-2290204	A	19991122		
	US 2000-216357P	P	20000705		
	WO 2000-CA1377	W	20001117		
AB	This invention provides a method for detection of multiple kinases or multiple kinase substrates, whereby the presence and phosphorylation state of a large no. kinases and/or kinase substrate proteins may be tracked in a single sample electrophoretically sepg. in one dimension, proteins in a sample to be tested for kinase or kinase substrate content; to produce an array of proteins so sepd. contacting the array with two or more antibodies selected from anti-kinase and anti-kinase substrate antibodies; and, detecting the presence of said antibodies bound to kinases or kinase substrate moieties in the array. This method may also comprise recording one or more values representative of a location for each of said detected antibodies bound to proteins in the array indicative of a location of a kinase or kinase substrate in the array.				
ST	multiblot kinase analysis				
IT	Information systems (data; multiblot kinase anal.)				
IT	Immunoassay (immunoblotting; multiblot kinase anal.)				
IT	Electrophoresis Membranes, nonbiological Mixtures Photographic films Polyacrylamide gel electrophoresis Recording Samples (multiblot kinase anal.)				
IT	Proteins, general, analysis FL: ANT (Analyte); ANST (Analytical study) (multiblot kinase anal.)				
IT	Antibodies FL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses) (multiblot kinase anal.)				
IT	Phosphorylation, biological (protein; multiblot kinase anal.)				
IT	Information systems (storage; multiblot kinase anal.)				
IT	9031-44-1, Kinase (phosphorylating) FL: ANT (Analyte); ANST (Analytical study) (multiblot kinase anal.)				
IT	96-65-5, 5'-ATP, uses FL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses) (multiblot kinase anal.)				
IT	9025-75-6, Phosphoprotein phosphatase FL: ARU (Analytical role, unclassified); CAT (Catalyst use); ANST (Analytical study); USES (Uses) (multiblot kinase anal.)				
IT	79-06-1, Acrylamide, uses 119-26-9, Bisacrylamide FL: NUU (Other use, unclassified); USES (Uses) (multiblot kinase anal.)				

L43 ANSWER 12 OF 16 HCAPLUS COPYRIGHT 2003 ACS

AN 2000:551303 HCAPLUS

DN 133:161561

TI Apparatus for supporting **protein** analysis, and memory medium
accommodating program for computer treatment with this apparatus

IN Kitajima, Masato; Oya, Michihiro

FA Fujitsu Ltd., Japan

SO Jpn. Kokai Tokkyo Koho, 10 pp.

CODEN: JKEXAF

DT Patent

LA Japanese

IC ICM G06F017-30

ICS G01N033-48; G01N033-566

CC 9-1 (Biochemical Methods)

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	JP 2000222421	A2	20000811	JP 1999-22997	19990129
	JP 3370942	B2	20030127		
PRAI	JP 1999-22997		19990129		

AB An app. for supporting **protein** anal. is designed so that the amino acid residue parts of a **protein** interacting with a low mol. wt. compd. are extd. in the form contg. the max. quantity of information on the structure of the **protein**. Using information from database (e.g., **Protein** Data Bank(PDB)), the amino acid residues contg. a specified kind of atom in the specified **protein** present within a certain distance from a resp. specified kind of atom in the specified compd. are searched. Then, a sequence pattern is formed by putting each amino acid residue obtained as a result of the search according to the certain notation rule in the order of the primary sequence of amino acid residues constituting the specified **protein**. This sequence pattern is made available as the information expressing the primary sequence structure at the part of the **protein** contg. the amino acid residue part interacting with the specified compd. A flow chart describing the treatment procedures for forming motif pattern is given.

ST **protein** analysis amino acid sequence database

IT Apparatus

Computer program

Databases

Memory devices

Nomenclature, general

Protein sequences

(app. for supporting **protein** anal., and memory medium
accommodating program for computer treatment with app.)

IT **Proteins**, general, biological studies

FL: BSU (Biological study, unclassified); PRF (Properties); BIOL
(Biological study)

(app. for supporting **protein** anal., and memory medium
accommodating program for computer treatment with app.)

IT **Information systems**

(data; app. for supporting **protein** anal., and
memory medium accommodating program for computer treatment with app.)

IT Amino acids, biological studies

FL: BSU (Biological study, unclassified); PRF (Properties); BIOL
(Biological study)

(residues; app. for supporting **protein** anal., and memory
medium accommodating program for computer treatment with app.)

L43 ANSWER 14 OF 16 HCAPLUS COPYRIGHT 2003 ACS

AN 2000:176020 HCAPLUS

DN 133:203124

TI Method for the rapid screening of drug candidates or other analytes

IN Pauwels, Rudi Wilfried Jan; Beelant, Christiaan Hubert Simon; Van Acker,
Koenraad Lodewijk August
PA Tibotec N.V., Belg.
SO PCT Int. Appl., 63 pp.
CODEN: PINKD2
DT Patent
LA English
IC ICM G01N033-543
ICS B01N003-02; G01N033-569; G01N033-573; C12Q001-18
CC 1-1 (Pharmacology)
Section cross-reference(s): 3, 9, 15

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 1998-014340	A1	19980316	WO 1998-1B1399	19980908
	W: AU, BF, CA, CN, IL, JP, KP, MX, NZ, PL, RU, SG, TR, US				
	FW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	CA 2342527	AA	19980316	CA 1998-1361627	19980908
	AU 2000021512	A5	19980327	AU 2000-22512	19980908
	BR 9216000	A	19980605	BR 1998-16000	19980908
	EP 1111494	A1	19980704	EP 1998-940489	19980908
	E: AT, BF, CH, DE, DK, ES, FR, GB, GR, IT, LU, NL, SE, PT, IE, FI				
	EP 1250955	A1	19981013	EP 2001-201142	19980908
	E: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LU, NL, SE, PT, IE, FI, CY				
	JP 2003517575	T2	20030527	JP 2000-569234	19980908
	TW 409312	B	20010411	TW 2000-8910.946	20000221
	ZA 2000000891	A	20000913	ZA 2000-891	20000223
	US 2002081629	A1	20020627	US 2001-25391	20011219
PRAI	EP 1998-940489	A3	19980908		
	WO 1998-1B1399	A	19980908		
	US 2000-569234	A3	20000630		
AB	A method for the rapid screening of analytes, e.g. potential drug candidates, comprises the steps of applying a plurality of analytes to be screened onto one or more solid support(s) such that the analytes remain isolated from one another; contacting the analyte-carrying solid support(s) with targets provided in a semi-solid or liq. medium, whereby the analytes are released from the solid support(s) to the targets; and measuring analyte-target interactions. This method allows for the manipulation of thousands of different analytes simultaneously. When the analyte is applied to the solid support, it can diffuse thereon so as to produce a concn. gradient and serial diln. of analyte if a dose response curve for a candidate drug is required. The method described can be readily automated.				
ST	drug analyte screening method app; automated drug analyte screening method app				
IT	Animal cell line (MT-4; rapid screening method for drug candidates or other analytes)				
IT	Liposomes (and beads; rapid screening method for drug candidates or other analytes)				
IT	Analysis Analysis Process automation Process automation (automated anal.; rapid screening method for drug candidates or other analytes)				
IT	Eukaryote (Eukaryotae) Prokaryote (cell; rapid screening method for drug candidates or other analytes)				
IT	Information systems (electronic or magnetic or digitized; rapid screening method for drug				

- candidates or other analytes)
 IT **Proteins**, specific or class
 PL: BPP (Biological process); BSU (Biological study, unclassified); BIOL
 (Biological study); PROC (Process)
 (green fluorescent; rapid screening method for drug candidates or other
 analytes)
- IT Pens
 (including plotter pens; rapid screening method for drug candidates or
 other analytes)
- IT Spectroscopy
 (lumimetry; rapid screening method for drug candidates or other
 analytes)
- IT Monolayers
 (mol. or cellular; rapid screening method for drug candidates or other
 analytes)
- IT Containers
 (print head; rapid screening method for drug candidates or other
 analytes)
- IT Analysis
 Analytical apparatus
 Antiviral agents
 Capillary tubes
 Cell
 Ceramics
 Charge coupled devices
 Colorimetry
 Containers
 Conveyor belts
 Densitometry (optical)
 Diffusion
 Drug screening
 Films
 Fluorescence microscopy
 Fluorometry
 Human immunodeficiency virus 1
 Immobilization, biochemical
 Langmuir-Blodgett films
 Membranes, nonbiological
 Microscopy
 Microtiter plates
 Molecules
Optical ROM disks
 Photographic films
Physical properties
 Radiochemical analysis
 Sensors
 Smart materials
 Virus
 (rapid screening method for drug candidates or other analytes)
- IT Antibodies
 Antigens
 Probes (nucleic acid)
 PL: ANT (Analyte); ANST (Analytical study)
 (rapid screening method for drug candidates or other analytes)
- IT Gelatins, uses
 PL: DEV (Device component use); USES (Uses)
 (rapid screening method for drug candidates or other analytes)
- IT Glass, uses
 PL: DEV (Device component use); USES (Uses)
 (rapid screening method for drug candidates or other analytes)
- IT Metals, uses
 PL: DEV (Device component use); USES (Uses)
 (rapid screening method for drug candidates or other analytes)

IT Polymers, uses
 FL: DEV (Device component use); USES (Uses)
 (rapid screening method for drug candidates or other analytes)

IT Polysaccharides, uses
 FL: DEV (Device component use); USES (Uses)
 (rapid screening method for drug candidates or other analytes)

IT Materials
 (tapes; rapid screening method for drug candidates or other analytes)

IT Receptors
 FL: PPF (Biological process); BSU (Biological study, unclassified); PEP
 (Physical, engineering or chemical process); BIOL (Biological study); PROC
 (Process)
 (target; rapid screening method for drug candidates or other analytes)

IT Containers
 (tubes; rapid screening method for drug candidates or other analytes)

IT 9063-38-6, Reverse transcriptase
 FL: BSU (Biological study, unclassified); BIOL (Biological study)
 (inhibitors; rapid screening method for drug candidates or other
 analytes)

IT 1461-15-0, Calcein
 FL: ARE (Analytical reagent use); ANST (Analytical study); USES (Uses)
 (rapid screening method for drug candidates or other analytes)

IT 30510-17-1, ACT 134678-17-4, FIC 147362-17-0, Ioviride
 FL: PAE (Biological activity or effector, except adverse); BSU (Biological
 study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES
 (Uses)
 (rapid screening method for drug candidates or other analytes)

IT 9002-18-0, Agar 9003-03-8, Polyacrylamide 9003-51-6, Polystyrene
 9004-34-6, Cellulose, uses 9004-67-5, Methylcellulose 9012-36-6,
 Agarose
 FL: DEV (Device component use); USES (Uses)
 (rapid screening method for drug candidates or other analytes)

IT 7631-86-9, Silicon dioxide, uses
 FL: DEV (Device component use); USES (Uses)
 (wafer; rapid screening method for drug candidates or other analytes)

RE.CNT 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD

RE

- (1) Andres, B; WO 9411571 A 1996 HCAPLUS
- (2) Burstein Lab Inc; WO 9401533 A 1998 HCAPLUS
- (3) Du Pont; GB 2008767 A 1979 HCAPLUS
- (4) Ekins, R; ANNALES DE BIOLOGIE CLINIQUE 1992, V50(5), P337 HCAPLUS
- (5) Leaback, D; US 4276048 A 1981 HCAPLUS
- (6) Pharmacopeia Inc; WO 9716569 A 1997 HCAPLUS
- (7) Sigal, N; COMB CHEM MOL DIVERSITY DRUG DISCOVERY F403

L43 ANSWER 15 OF 16 HCAPLUS COPYRIGHT 2003 ACS

AN 1989:456544 HCAPLUS

DN 111:56544

TI An electronic database for molecular biology

AJ Burridge, Jane M.

CS IEM, Winchester/Hants., SO23 8PX, UK

SO Biochemical Society Transactions (1989), 17(5), 840-1

CODEN: BCSTB5; ISSN: 0950-5127

DT Journal

LA English

CC 10-5 (History, Education, and Documentation)

Section cross-reference(s): 6

AB The development of a compact disk-read only memory (CD-ROM) mol. database is described which will make numerical data, text, graphics, and images available to be browsed, searched, and manipulated interactively. The CD-ROM publication will hold numerical data defining 400 or so large **protein** mols. together with several hundred high-resoln. color pictures depicting these mols., several key texts describing properties,

regularities, and peculiarities of the mols., and some programs.

ST **protein** compact disk format database
 IT **Proteins**, uses and miscellaneous
 FI: USES (Uses)
 (database of, compact disk-read only memory format of, development of)
 IT **Memory devices**
 (optical, disks, read-only,
protein database on format of, development of)
 IT **Information science and technology**
 (system, computerized, of **proteins**,
 compact disk-read only memory format of, development of)

L43 ANSWER 16 OF 16 HCAPLUS COPYRIGHT 2003 ACS

AN 1987:570984 HCAPLUS

DI 107:170984

TI A DNA and **protein** database system on CD-ROM

AD Nasu, Hisanori; Itoh, Toshiaki

CS Hitachi Software Eng. Co., Ltd., Yokohama, 231, Japan

SO Joho Kanri (1986), 29(3), 657-66

CODEN: JOKAAB; ISSN: 0021-7293

DT Journal

LA Japanese

CC 6-7 (General Biochemistry)

Section cross-reference(s): 3, 10

AB ENASIS-DEFEF31 is an information storage and retrieval system for DNA and **protein** ref. and sequence data. The data and software are loaded on CD-ROM. The system can be run on Hitachi B-16, NEC PC 9801 series or IBM PC-XT/AT personal computers. The source files of the database are GenBank, EMBL, and NBRF. The system has capabilities for retrieval of ref. information as well as homol. searching for sequence data.

ST CD ROM DNA **protein** sequence database

IT Deoxyribonucleic acid sequences

Protein sequences

(database of, on CD-ROM)

IT **Memory devices**

(optical, disks, read-only, DNA
 and **protein** databases on)

IT **Information science and technology**

(system, computerized, for DNA and **protein**
 sequences, on CD-ROM)

= d all tot

L47 ANSWER 1 OF 6 HCAPLUS COPYRIGHT 2003 ACS

AN 2002:869628 HCAPLUS

DI 137:334941

TI Analysis mechanism for genetic data

IN Hytopoulos, Evangelos; Miller, Brett; Ray, Sandip

EA E-Mine, USA

SO U.S. Pat. Appl. Publ., 34 pp.

CODEN: USXXCO

DT Patent

LA English

IC ICM G06F019-00

ICS G01N033-48; G01N033-50

NCL 702019000

CC 9-16 (Biochemical Methods)

Section cross-reference(s): 3

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
FI	US 2002169560	A1	20021114	US 2001-854427	20010512

PRAI US 2001-854427 20010512
 AB Results of statistical **clustering** and/or correlation anal. of genetic or proteomic expression data such as microarrays, gene chips, or **protein** chips are used, e.g., as response variables, in further anal. of expression data. In particular, an array of expression data is **clustered** using a **cluster** tool to produce an array of expression **clusters**. Each of the expression **clusters** represents the same expts. represented by the original expression array. Accordingly, each **cluster** of the array is of the proper form to be used as a response variable of expression values. Using an expression **cluster** as a response variable for either supervising **clustering** or correlation anal. allows correlation between such an expression **cluster** and other expression data.

ST analysis mechanism genetics
 IT **Cluster analysis**
 Computer application
 Computers
 Configuration
 Correlation analysis
 DNA microarray technology
 Gene expression profiles
 Genetics
 Memory devices
 Microarray technology
 Protein microarray technology
 (anal. mechanism for genetic data)

IT Gene
 Proteins
 Proteome
 FL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
 (anal. mechanism for genetic data)

IT **Information systems**
 (data; anal. mechanism for genetic data)

IT Education
 (instructions; anal. mechanism for genetic data)

L47 ANSWER 3 OF 6 HCAPLUS COPYRIGHT 2003 ACS
 AN 2002:450025 HCAPLUS
 DI 127:16492
 TI Computer-based **cluster** analysis of gene expression patterns
 IN Kobayashi, Takeshi; Honda, Hiroyuki; Hanai, Taizou; Tomita, Shuta
 PA Nagoya Industrial Science Research Institute, Japan
 SO ECT Int. Appl., 134 pp.
 COBEN: PINKD2
 DT Patent
 LA Japanese
 IC ICM G06F017-20
 ICS C12N015-00
 CC 3-1 (Biochemical Genetics)
 Section cross-reference(s): 9, 20

FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002046962	A1	20020613	WO 2001-JF10704	20011206
W: AE, AG, AL, AM, AT, AU, AZ, BA, BE, BG, BF, BY, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DO, EC, EE, ES, FI, GB, GD, GE, GH, GM, HE, HU, ID, IL, IN, IS, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, ME, NO, NE, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, UA, UG, US, VE, VN, YU, ZA, ZW, AA, AB, AC, AD, AE, AF, AG, AH, AI, AJ, AK, AL, AM, AN, AO, AP, AQ, AR, AS, AT, AU, AV, AW, AX, AY, AZ, BA, BB, BC, BD, BE, BF, BG, BH, BI, BJ, BK, BL, BM, BN, BO, BP, BQ, BR, BS, BT, BU, BV, BW, BX, BY, BZ, CA, CB, CC, CD, CE, CF, CG, CH, CI, CJ, CK, CL, CM, CN, CO, CP, CQ, CR, CS, CT, CU, CV, CW, CX, CY, CZ, DA, DB, DC, DD, DE, DF, DG, DH, DI, DJ, DK, DL, DM, DN, DO, DP, DQ, DR, DS, DT, DU, DV, DW, DX, DY, DZ, EA, EB, EC, ED, EE, EF, EG, EH, EI, EJ, EK, EL, EM, EN, EO, EP, EQ, ER, ES, ET, EU, EV, EW, EX, EY, EZ, FA, FB, FC, FD, FE, FF, FG, FH, FI, FJ, FK, FL, FM, FN, FO, FP, FQ, FR, FS, FT, FU, FV, FW, FX, FY, FZ, GA, GB, GC, GD, GE, GF, GH, GI, GJ, GK, GL, GM, GN, GO, GP, GQ, GR, GS, GT, GU, GV, GW, GX, GY, GZ, HA, HB, HC, HD, HE, HF, HG, HH, HI, HJ, HK, HL, HM, HN, HO, HP, HQ, HR, HS, HT, HU, HV, HW, HX, HY, HZ, IA, IB, IC, ID, IE, IF, IG, IH, II, IJ, IK, IL, IM, IN, IO, IP, IQ, IR, IS, IT, IU, IV, IW, IX, IY, IZ, JA, JB, JC, JD, JE, JF, JG, JH, JI, JJ, JK, JL, JM, JN, JO, JP, JQ, JR, JS, JT, JU, JV, JW, JX, JY, JZ, KA, KB, KC, KD, KE, KF, KG, KH, KI, KJ, KK, KL, KM, KN, KO, KP, KQ, KR, KS, KT, KU, KV, KW, KX, KY, KZ, LA, LB, LC, LD, LE, LF, LG, LH, LI, LJ, LK, LM, LN, LO, LP, LQ, LR, LS, LT, LU, LV, LW, LX, LY, LZ, MA, MB, MC, MD, ME, MF, MG, MH, MI, MJ, MK, ML, MN, MO, MP, MQ, MR, MS, MT, MU, MV, MW, MX, MY, MZ, NA, NB, NC, ND, NE, NF, NG, NH, NI, NJ, NK, NL, NM, NO, NP, NQ, NR, NS, NT, NU, NV, NW, NX, NY, NZ, OA, OB, OC, OD, OE, OF, OG, OH, OI, OJ, OK, OL, OM, ON, OO, OP, OQ, OR, OS, OT, OU, OV, OW, OX, OY, OZ, PA, PB, PC, PD, PE, PF, PG, PH, PI, PJ, PK, PL, PM, PN, PO, PP, PQ, PR, PS, PT, PU, PV, PW, PX, PY, PZ, QA, QB, QC, QD, QE, QF, QG, QH, QI, QJ, QK, QL, QM, QN, QO, QP, QQ, QR, QS, QT, QU, QV, QW, QX, QY, QZ, RA, RB, RC, RD, RE, RF, RG, RH, RI, RJ, RK, RL, RM, RN, RO, RP, RQ, RR, RS, RT, RU, RV, RW, RX, RY, RZ, SA, SB, SC, SD, SE, SF, SG, SH, SI, SJ, SK, SL, SM, SN, SO, SP, SQ, SR, SS, ST, SU, SV, SW, SX, SY, SZ, TA, TB, TC, TD, TE, TF, TG, TH, TI, TJ, TK, TL, TM, TN, TO, TP, TQ, TR, TS, TU, TV, TW, TX, TY, TZ, UA, UB, UC, UD, UE, UF, UG, UH, UI, UJ, UK, UL, UM, UN, UO, UP, UQ, UR, US, UT, UV, UW, UX, UY, UZ, VA, VB, VC, VD, VE, VF, VG, VH, VI, VJ, VK, VL, VM, VN, VO, VP, VQ, VR, VS, VT, VU, VV, VW, VX, VY, VZ, WA, WB, WC, WD, WE, WF, WG, WH, WI, WJ, WK, WL, WM, WN, WO, WP, WQ, WR, WS, WT, WU, WV, WW, WX, WY, WZ, XA, XB, XC, XD, XE, XF, XG, XH, XI, XJ, XK, XL, XM, XN, XO, XP, XQ, XR, XS, XT, XU, XV, XW, XX, XY, XZ, YA, YB, YC, YD, YE, YF, YG, YH, YI, YJ, YK, YL, YM, YN, YO, YP, YQ, YR, YS, YT, YU, YV, YW, YX, YY, YZ, ZA, ZB, ZC, ZD, ZE, ZF, ZG, ZH, ZI, ZJ, ZK, ZL, ZM, ZN, ZO, ZP, ZQ, ZR, ZS, ZT, ZU, ZV, ZW, ZX, ZY, ZZ				
LW: GR, GM, GE, LS, MW, ME, SO, SL, SZ, TZ, US, SM, SW, AT, BE, CH, CY, DE, EK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR,				

BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MP, NE, SN, TD, TG
 JP 2001175206 A2 20020621 JP 2000-372765 20001208
 AU 2002031076 A5 20020618 AU 2002-11076 20011206
 PFAI JP 2000-372765 A 20001208
 WO 2001-JP10704 W 20011206
 AB A method and app. for **clustering** anal. of data for gene expression patterns using computer programs and computer readable memory storage device, are disclosed. Genes are **clustered** by acquiring **signal** patterns showing the expression states of the genes and then processing the **signal** patterns thus acquired by using the ART technique. Examn. of gene expression patterns in *Saccharomyces cerevisiae* wild type using Fuzzy ART program is described. Data are displayed in groups.
 ST gene expression **cluster** analysis computer program
 IT **Computer program**
 (ART, Fuzzy ART; computer-based **cluster** anal. of gene expression patterns)
 IT **Bioinformatics**
Cluster analysis
Computer application
 Computers
Magnetic memory devices
 (computer-based **cluster** anal. of gene expression patterns)
 IT Gene
 FL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
 (expression; computer-based **cluster** anal. of gene expression patterns)
 RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD
 RE
 (1) Frank, T; IEEE TRANSACTIONS ON NEURAL NETWORKS 1994, V9(3), P544
 (2) Hiraishi, A; Nippon Biseibutsu Seital Gakkaiho 1995, V10(3), P119
 (3) Tsujimoto, G; Chapter 2: Transcript-.mu.m Kaseki; IV Bio Informatics; 1 Transcript-.mu.m Informatics 2000, P121
 L47 ANSWER 3 OF 6 HCAPLUS COPYRIGHT 2003 ACS
 AN 2002:241116 HCAPLUS
 DN 136:258302
 TI Phylogenetic tree diagram display for gene expression data **cluster** analysis
 IN Horaki, Yasuyuki; Nakashige, Fyo; Tamura, Takur
 PA Hitachi Software Engineering Co., Ltd., Japan
 SO PCT Int. Appl., 49 pp.
 CODEN: BINXD2
 DT Patent
 LA Japanese
 IC ICM G06F017-30
 ICS G06F019-00; G01N033-50; G1L0015-11
 CC 3-1 (Biochemical Genetics)
 Section cross-reference(s): 9, 20
 FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2002025489	A1	20020318	WO 2000-JP6385	20000919
W: JP, US				
FW: EE, FR, GB				

 PRAI WO 2000-JP6385 20000919
 AB A system of **cluster** anal. for gene expression data from DNA microarray hybridization is described that uses std. statistical algorithms to arrange genes according to similarity in pattern of gene expression. The output is displayed graphically, in the form of phylogenetic tree diagram, conveying the **clustering** and the underlying expression data simultaneously in a form intuitive for

biologists. A threshold indicating a similarity of expression patterns is preset, and genes with the same function and genes similar in expression pattern to those genes are extd. and displayed. In addn., an expt. pattern required by **clustering** is reselected for the extd. genes and is then used to subject them to **cluster** anal. How many individual functions are available in genes belonging to a partial tree is calcd. to det. ratios in which individual functions account for in a partial tree. If their ratios in the partial tree exceed the preset threshold, they are regarded as a **cluster** (set of genes similar in function) and are subjected to extn. processing.

ST evolution tree diagram computer graphic display genetics **cluster** analysis; **cluster** analysis genome expression DNA microarray hybridization

IT Audiovisual aids
(diagrams; phylogenetic tree diagram display for gene expression data **cluster** anal.)

IT Gene
RE: BSU (Biological study, unclassified); BGL (Biological study)
(expression; phylogenetic tree diagram display for gene expression data **cluster** anal.)

IT Evolution
(mol.; phylogenetic tree diagram display for gene expression data **cluster** anal.)

IT Bioinformatics
Cluster analysis
Computer application
Computer program
DNA microarray technology
Information, biological
Magnetic memory devices
(phylogenetic tree diagram display for gene expression data **cluster** anal.)

PE.CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD

FE

- (1) Fujitsu Limited; JP 07-274965 A 1997
- (2) Fujitsu Limited; GB 2283840 A 1997
- (3) Fujitsu Limited; US 5598350 A 1997
- (4) Boss, D; Nature Genetics 2000, V24(3), P227 HCAPLUS

L47 ANSWER 4 OF 6 HCAPLUS COPYRIGHT 2003 ACS

AN 2001:741258 HCAPLUS

DN 135:283937

TI Computer-based **cluster** analysis and display of gene expression patterns

IN Nakashige, Akira; Nozaki, Yasuyuki; Watanabe, Tsunehiko; Tamura, Takao

PA Hitachi Software Engineering Co., Ltd., Japan

SD Jpn. Kohai Tokkyo Koho, 10 pp.

COLEN: JKNXAF

DT Patent

LA Japanese

PC JCN G01N033-53

ICS G11M001-00; G01N033-566; G01N035-00; G01N035-02; G01N037-00;
G11N015-09

CC 4-1 (Biochemical Genetics)

Section cross-reference(s): 9, 20

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
FI	JP 2001281244	AL	20011010	JP 2000-33695	20000328
PRAI	JP 2000-88695		20000328		
AB	A method and materials for graphic display of data on gene expression patterns obtained via clustering anal. using computer programs and computer readable memory storage device, are disclosed. Data are				

ST displayed in groups.
gene expression **cluster** analysis computer program graphic display

IT **Bioinformatics**
Cluster analysis
Computer application
Computer program
Computers
Magnetic memory devices
(computer-based **cluster** anal. and display of gene expression patterns)

IT Gene
(expression; computer-based **cluster** anal. and display of gene expression patterns)

L47 ANSWER 5 OF 6 HCAPLUS COPYRIGHT 2002 ACS
AN 2001:507491 HCAPLUS
DI 135:89544
TI Database system and method useful for predicting putative ligand binding sites
IN Edelman, Marvin; Kuttner, Yosef; Sebolev, Vladimir
PA Yeda Research and Development Co. Ltd., Israel
SO PCT Int. Appl., 49 pp.
CODEN: PIKXD2
DT Patent
LA English
IC ICM A61K
CC 9-16 (Biochemical Methods)
Section cross-reference(s): 6, 7, 20

FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001049244	A2	20010712	WO 2001-119	20010102
WO 2001049244	A3	20020307		

W: AE, AG, AL, AM, AT, AU, AV, BA, BB, BC, BD, BE, BF, BG, BH, BI, BJ, BK, BL, BM, BN, BO, BP, BQ, BR, BS, BT, BU, BV, BW, BX, BY, BZ, CA, CH, CN, CO, CP, CU, CV, CW, CX, CY, CZ, DA, DB, DC, DD, DE, DF, DG, DH, DI, DJ, DK, DL, DM, DN, DO, DP, DQ, DR, DS, DT, DU, DV, DW, DX, DY, DZ, EA, EB, EC, ED, EE, EF, EG, EH, EI, EJ, EK, EL, EM, EN, EO, EP, EQ, ER, ES, ET, EU, EV, EW, EX, EY, EZ, FA, FB, FC, FD, FE, FF, FG, FH, FI, FJ, FK, FL, FM, FN, FO, FP, FQ, FR, FS, FT, FU, FV, FW, FX, FY, FZ, GA, GB, GC, GD, GE, GF, GH, GI, GJ, GK, GL, GM, GN, GO, GP, GQ, GR, GS, GT, GU, GV, GW, GX, GY, GZ, HA, HB, HC, HD, HE, HF, HG, HH, HI, HJ, HK, HL, HM, HN, HO, HP, HQ, HR, HS, HT, HU, HV, HW, HX, HY, HZ, IA, IB, IC, ID, IE, IF, IG, IH, II, IJ, IK, IL, IM, IN, IO, IP, IQ, IR, IS, IT, IU, IV, IW, IX, IY, IZ, JA, JB, JC, JD, JE, JF, JG, JH, JI, JJ, JK, JL, JM, JN, JO, JP, JQ, JR, JS, JT, JU, JV, JW, JX, JY, JZ, KA, KB, KC, KD, KE, KF, KG, KH, KI, KJ, KK, KL, KM, KN, KO, KP, KQ, KR, KS, KT, KU, KV, KW, KX, KY, KZ, LA, LB, LC, LD, LE, LF, LG, LH, LI, LJ, LK, LL, LM, LN, LO, LP, LQ, LR, LS, LT, LU, LV, LW, LX, LY, LZ, MA, MB, MC, MD, ME, MF, MG, MH, MI, MJ, MK, ML, MN, MO, MP, MQ, MR, MS, MT, MU, MV, MW, MX, MY, MZ, NA, NB, NC, ND, NE, NF, NG, NH, NI, NJ, NK, NL, NM, NO, NP, NQ, NR, NS, NT, NU, NV, NW, NX, NY, NZ, OA, OB, OC, OD, OE, OF, OG, OH, OI, OJ, OK, OL, OM, ON, OO, OP, OQ, OR, OS, OT, OU, OV, OW, OX, OY, OZ, PA, PB, PC, PD, PE, PF, PG, PH, PI, PJ, PK, PL, PM, PN, PO, PP, PQ, PR, PS, PT, PU, PV, PW, PX, PY, PZ, QA, QB, QC, QD, QE, QF, QG, QH, QI, QJ, QK, QL, QM, QN, QO, QP, QQ, QR, QS, QT, QU, QV, QW, QX, QY, QZ, RA, RB, RC, RD, RE, RF, RG, RH, RI, RJ, RK, RL, RM, RN, RO, RP, RQ, RR, RS, RT, RU, RV, RW, RX, RY, RZ, SA, SB, SC, SD, SE, SF, SG, SH, SI, SJ, SK, SL, SM, SN, SO, SP, SQ, SR, SS, ST, SU, SV, SW, SX, SY, SZ, TA, TB, TC, TD, TE, TF, TG, TH, TI, TJ, TK, TL, TM, TN, TO, TP, TQ, TR, TS, TU, TV, TW, TX, TY, TZ, UA, UB, UC, UD, UE, UF, UG, UH, UI, UJ, UK, UL, UM, UN, UO, UP, UQ, UR, US, UT, UV, UW, UX, UY, UZ, VA, VB, VC, VD, VE, VF, VG, VH, VI, VJ, VK, VL, VM, VN, VO, VP, VQ, VR, VS, VT, VU, VV, VW, VX, VY, VZ, WA, WB, WC, WD, WE, WF, WG, WH, WI, WJ, WK, WL, WM, WN, WO, WP, WQ, WR, WS, WT, WU, WV, WW, WX, WY, WZ, XA, XB, XC, XD, XE, XF, XG, XH, XI, XJ, XK, XL, XM, XN, XO, XP, XQ, XR, XS, XT, XU, XV, XW, XX, XY, XZ, YA, YB, YC, YD, YE, YF, YG, YH, YI, YJ, YK, YL, YM, YN, YO, YP, YQ, YR, YS, YT, YU, YV, YW, YX, YY, YZ, ZA, ZB, ZC, ZD, ZE, ZF, ZG, ZH, ZI, ZJ, ZK, ZL, ZM, ZN, ZO, ZP, ZQ, ZR, ZS, ZT, ZU, ZV, ZW, ZX, ZY, ZZ.

FW: GH, GM, KE, LS, MW, MZ, SD, SL, SE, TC, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LG, MC, NL, PT, SE, TR, BF, RI, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRAI IL 2000-133866 A 20000103

AB A method of identifying at least one consensus structural characteristic of binding sites of a ligand of interest is provided. The method is effected by: (a) obtaining structural data pertaining to a plurality of **proteins** while complexed with the ligand of interest; and (b) extg. from the structural data at least one consensus structural characteristic characterizing an interaction between the ligand of interest and at least one of the plurality of **proteins**, thereby identifying at least one consensus structural characteristic of binding sites of the ligand of interest. The process for identification of a consensus structural characteristic of binding sites for ATP is described. A non-redundant dataset of **protein/ATP** complexes was prepd. and used.

ST database system predicting ligand binding site **protein** structure; ATP binding site **protein** consensus structure

IT **Algorithm**
(**CLUSTER**; database system and method useful for predicting putative ligand binding sites)

IT Heat-shock **proteins**
EL: BEF (Biological process); BSU (Biological study, unclassified); PRP

- (Properties); BIOL (Biological study); PPOC (Process)
(HSP 70, 44-kD N-terminal fragment, as ATP-binding **protein**;
database system and method useful for predicting putative ligand
binding sites)
- IT Insulin receptors
Myosins
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP
(Properties); BIOL (Biological study); PPOC (Process)
(as ATP-binding **proteins**; database system and method useful
for predicting putative ligand binding sites)
- IT **Optical disks**
(computer; database system and method useful for predicting putative
ligand binding sites)
- IT **Information systems**
(data; database system and method useful for predicting
putative ligand binding sites)
- IT **Proteins, general, properties**
RL: BPR (Properties)
(database PDB; database system and method useful for predicting
putative ligand binding sites)
- IT Apparatus
Cluster analysis
Computer program
Computers
Data processing
Databases
Magnetic memory devices
Optical memory devices
(database system and method useful for predicting putative ligand
binding sites)
- IT Ligands
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP
(Properties); BIOL (Biological study); PPOC (Process)
(database system and method useful for predicting putative ligand
binding sites)
- IT **Optical disks**
(digital video disk (DVD); database system and method useful for
predicting putative ligand binding sites)
- IT Structure-activity relationship
(ligand-binding; database system and method useful for predicting
putative ligand binding sites)
- IT **Proteins, specific or class**
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP
(Properties); BIOL (Biological study); PPOC (Process)
(ligand-binding; database system and method useful for predicting
putative ligand binding sites)
- IT **Magnetic disks**
Optical disks
(magneto-optical disks; database system and method useful for predicting
putative ligand binding sites)
- IT **Information systems**
(network; database system and method useful for predicting
putative ligand binding sites)
- IT Actins
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP
(Properties); BIOL (Biological study); PPOC (Process)
(profilactins, .beta.-actin, as ATP-binding **proteins**;
database system and method useful for predicting putative ligand
binding sites)
- IT **Information systems**
(storage; database system and method useful for predicting
putative ligand binding sites)
- IT Actins

RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PPOC (Process)
(.beta.-, complexes with profilin, as ATP-binding **proteins**;
database system and method useful for predicting putative ligand binding sites)

IT 52600-18-1
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PPOC (Process)
(.alpha.-subunit or 1, as ATP-binding **protein**; database system and method useful for predicting putative ligand binding sites)

IT 9001-88-6, Phosphoglycerate kinase 9001-88-1, Phosphorylase kinase 9012-49-1, Aspartate transcarbamylase 9013-02-0, Adenylate kinase 9032-68-3, NAD synthetase 9073-94-3, Phosphoenolpyruvate carboxykinase 141349-86-2, cyclin-dependent kinase 2 142048-39-5, cAMP-dependent **protein** kinase 145539-86-2, Hematopoietic cellular kinase
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PPOC (Process)
(as ATP-binding **protein**; database system and method useful for predicting putative ligand binding sites)

IT 56-65-5, ATP, biological studies 56-65-5D, ATP, analogs, biological studies
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PPOC (Process)
(as ligand; database system and method useful for predicting putative ligand binding sites)

IT 35612-73-1
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PPOC (Process)
(database system and method useful for predicting putative ligand binding sites)

L47 ANSWER 6 OF 5 HCAELUS COPYRIGHT 2003 ACS

AN 1993:471898 HCAELUS

DN 119:71898

TI Substructure searching on very large files by using multiple storage techniques

AU Bartmann, Alexander; Maier, Helmut; Walkowiak, Dirk; Roth, Bernard; Hicks, Martin G.

CS Softron GmbH, Graefelfing, D8032, Germany

SO Journal of Chemical Information and Computer Sciences (1993), 33(4), 539-41

CODEN: JCISDH; ISSN: 0095-2338

DT Journal

LA English

CC 20-5 (History, Education, and Documentation)

AB Traditional substructure search systems use a 2-stage algorithm consisting of a preliminary screening which operates on (inverted) index files to det. a set of candidates to be processed by the atom-by-atom search (ABAS). The screening stage is usually fast, the performance of the system being governed by the screening efficiency. If a large no. of candidates is left after the screening, the result is often a very large increase in retrieval time. The ABAS becomes the time-dependent stage due to the excessively large no. of disk seeks required to get the randomly distributed structure records into memory. The new search algorithm described in this paper is based on a special preprocessed structure file. It contains multiples of each mol.'s connection table organized in **clusters** forming contiguous portions of the search file. Each **cluster** can be characterized by a substructure contained in all its mols. A mol. may be a member of several different **clusters**, or it may appear repeatedly in the same **cluster**. File generation and update is fast and simple, and the mass storage requirements are only approx. 1 kbyte/mol. A substructure search is performed by finding the min. set of **clusters** contg. all

candidates for a given query. The ABAS only has to scan sequentially through the relevant portions of the structure file. Furthermore, each single I/O-operation can read hundreds of structures into memory. Only the structures that are not already verified to be hits by the screening must be processed. The ABAS is CPU-bound. This architecture offers an extremely good performance on very large files for various computer platforms (e.g., IBM-PC, IBM-Mainframe, VAX) and even on slow storage devices like CD-ROMs.

ST storage technique searching mol substructure
 IT **Algorithm**
 (for mol. substructure searching on large files using multiple storage techniques)
 IT **Memory devices**
 (optical, disks, read-only, mol. substructure storage on, searching of)
 IT **Information science and technology**
 (searching, computerized, of mol. substructures, in large files using multiple storage techniques)
 IT **Information science and technology**
 (storage, of mol. substructures, for online searching)
 IT **Information science and technology**
 (storage, computerized, of mol. substructures, for online searching)
 IT Molecular structure
 (substructure, searching of, in large files using multiple storage techniques)

=> fil compuscie

FILE 'COMPUSCIE' ENTERED AT 11:08:09 ON 28 MAY 2003
 COPYRIGHT (c) 2003 FACHINFORMATIONSZENTRUM KARLSRUHE (FIZ KARLSRUHE)

FILE LAST UPDATED: 18 DEC 2002 <20021218/UF>
 FILE COVERS 1972 TO DATE.

=> d all

LIB3 ANSWER 1 OF 1 COMPUSCIE COPYRIGHT 2003 FIZ KARLSRUHE
 AN 1982(4):PH2022 COMPUSCIE
 TI Biophysical and biochemical information transfer in recognition.
 AU Editor(s): Vassileva-Popova, J.G.; Jensen, E.V.
 SO New York: Plenum Press. 1979. 692 p.
 Conference: 1. International Colloquium on Physical and Chemical
 Information Transfer in Regulation of Reproduction and Ageing (PCITRRA),
 Varna (Bulgaria), 2-8 Oct 1977
 ISBN: 0-306-40036-7
 DT Book; Conference
 CY United States
 LA English
 IP FIZKA
 AB In this issue, physical and chemical aspects of biological recognition are discussed. Mathematical approaches, models and hypotheses for studying biological recognition are involved. Further, application of physical and chemical aspects of biorecognition in development and ageing are included. An extraordinarily varied set of topics is to be found between the covers of this volume which contains the proceedings of the Colloquium-hormone activity and hormone receptors, cyclic AMP, membranes, microtubules, adenylate cyclase, the quantum mechanics of biological molecules, enzyme specificity and kinetics, brain peptides and proteins, prolactin, circadian rhythms, oscillatory reactions, and even such unorthodox investigations as the study of magnetic field effects and the

search for light guides in biological systems. So wide a range of investigation also requires new tools, and one section of the book is devoted to a discussion of new kinds of instrumentation - rapid spectrophotometers, lasers, and stopped-flow techniques. (orig.)

CC *B.4 Memory structures
ST BIOPHYSICS; HORMONES; ENZYMES; KININS; RECEPTORS; SPECIFICITY; AGING;
MUSCLES; CELL MEMBRANES; PERMEABILITY; LABELLING; AUTORADIOGRAPHY;
REPRODUCTION; MEMORY DEVICES; NERVOUS SYSTEM

= fil wpi*

FILE 'WPI*' ENTERED AT 11:16:49 ON 28 MAY 2003
COPYRIGHT (C) 2003 THOMSON DERWENT

FILE LAST UPDATED: 26 MAY 2003 020030516/UPD
MOST RECENT DERWENT UPDATE: 200373 02003037/DW>
DERWENT WORLD PATENTS INDEX SUBSCRIBER FILE, COVERS 1963 TO DATE

NEW WEEKLY SDI FREQUENCY AVAILABLE --> see NEWS <<<

SLAPT (Simultaneous Left and Right Truncation) is now available in the /ABEX field. An additional search field /BIX is also provided which comprises both /BI and /ABEX <<<

PATENT IMAGES AVAILABLE FOR PRINT AND DISPLAY <<<

FOR DETAILS OF THE PATENTS COVERED IN CURRENT UPDATES,
SEE <http://www.derwent.com/dwpi/updates/dwpiucv/index.html> <<<

FOR A COPY OF THE DERWENT WORLD PATENTS INDEX STN USER GUIDE,
PLEASE VISIT:
http://www.stn-international.de/training_center/patents/stn_guide.pdf <<<

FOR INFORMATION ON ALL DERWENT WORLD PATENTS INDEX USER
GUIDES, PLEASE VISIT:
http://www.derwent.com/userguides/dwpi_guide.html <<<

= d all abeq tech abex tot

LD0 ANSWER 1 OF 5 WPI* (C) 2003 THOMSON DERWENT

AN 2002-631531 [68] WPI*

INN N2002-499397 INC C2002-178497

TI Analysis of amino acid sequences and average characteristic values with continuous analytic parameters, to forecast structure and function of proteins.

DE B04 D10 S03 T01

FA (FUJIO-I) FUJIOH M; (MATS-I) MATSUOKA F; (TSUK-I) TSUKAHARA T

CYC 1

PI JP 200115635 A JP 20010802 (200168)* 19p G06F017-30 <--

AST JP 2002215635 A JP 2001-13859 20010122

PRAI JP 2001-13859 20010122

IC ICM G06F017-30

ICS G01N033-68; G06F019-00

ICA C12N015-09

AB JF2002215635 A UFAP: 20021012

NOVELTY - A distribution analysis of amino acid sequences for the forecast of structure and functions of a protein, is new.

DETAILED DESCRIPTION - A distribution analysis of amino acid sequences for the forecast of structure and functions of a protein by:

- (a) calculation of amino acid species based on the predetermined parameters for the read plural amino acid sequences;
- (b) drawing of an amino acid distribution pattern for the analyzed individual amino acids; and

(c) forecasting the structure and functions of the protein on the basis of amino acid distribution pattern, is new.

USE - The method is useful for the analysis of the amino acid sequence of a protein, to forecast its structure and function.

ADVANTAGE - The method provides an easily operable analysis of functions and structures of amino acid sequences with pattern recognition.

DESCRIPTION OF DRAWING(S) - The drawing shows a flow chart explaining the method.

- 11 an apparatus for the analysis of amino acid distribution
- 111 a procedure of input and selection
- 113 a procedure for the memory of amino acid sequence data
- 114 a procedure for the memory of parameters
- 115 reading of amino acid sequence
- 116 a procedure for counting amino acid species
- 117 a procedure for sorting the calculated values
- 118 a procedure for plotting the amino acid distribution pattern
- 119 amino acid distribution diagram
- 120 a procedure for calculation of each segment
- 121 a procedure for establishment of category
- 122 a procedure for plotting category distribution pattern
- 123 category distribution diagram

Dwg. 1/15

FS CFI EPI

EA AB; GI; DCN

MC CFI: B11-C08F3; B11-C08G; D05-H09

EPI: S03-E14H; T01-J; T01-J05B

ABEX UPTX: 10011822

EXAMPLE - No suitable example given.

L90 ANSWER 2 OF 5 WPIN (C) 2003 THOMSON DERWENT

AN 2002-608539 [65] WPIN

CR 2002-667079 [71]

DIN N2002-481830 DMC C2002-172137

TI Machine implemented method for deriving oligomer sequence from mass spectrum data, by providing predetermined set of mass/charge values for monomer sequences and determining abundance value for each monomer.

DC B04 D16 S03 T01 V05

IN HALL, M F; PETESCH, F; SCHNEIDER, L V

PA (TARGET-1) TARGET DISCOVERY INC

CYC 96

PI WO 2002061661 A2 20020808 (200265)* EN 151p G06F019-00 4--

FW: AT BE CH CY DE DK EA ES FI FR GE GH GM GR IE IT KE LS LU MC MW MZ

NL OA PT SD SE SL SZ TF TE UG ZW

W: AE AG AL AM AT AU BA BE BG BF BY CA CH CN CO CR CU CZ DE DK

DM DZ EC EE ES FI GB GL GE GR GM HF HG HD IL IN IS JP KE KG KP KR

KZ LC LK LF LS LT LU LV MA MD MG MK MN MW MX ME NO NZ PH PL PT RO

RU SB SE SG SI SK SL TC TM TR TT UA UG UZ VN YU ZA ZW

ADT WO 2002061661 A2 WO 2001-US49491 20011019

FFAI US 2000-242398P 10001019; US 2000-242165P 20001019

IC ICM G06F019-00

ICS G10Q001-68; G01N033-68; H01J049-00

AB WO 2002061661 A UFAB: 20021108

NOVELTY - A machine implemented method (M1) for deriving sequence of a portion of oligomer from mass spectrum data (MSD), comprising providing predetermined set (PDS) of mass/charge (m/z) values for monomer sequences (MS), determining abundance value from MSD for each m/z value in PDS, thus producing number of abundance values, calculating a first ranking, for each sequence of set of MS having first number of monomer.

DETAILED DESCRIPTION - A machine implemented method for deriving a sequence of a portion of oligomer from mass spectrum data (MSD), comprising:

(a) providing predetermined set of mass/charge (m/z) values for monomer sequences each of which comprises a mass label;

(b) determining abundance value from MSD for each m/z value in the predetermined set, thus producing number of abundance values; and
 (c) calculating a first ranking, based on abundance values, for each sequence of a set of monomer sequences having a first number of monomer.

INDEPENDENT CLAIMS are also included for the following:

(1) a machine readable medium containing executable computer program instructions, which when executed by a processing system cause the processing system to perform M1;

(2) processing (M2) noise in a mass spectrum data of a fragmented oligomer, comprising:

(a) determining a periodic block of noise in a mass spectrum data generated from accelerating fragments of an oligomer to a detector; and

(b) filtering the periodic block of noise from the mass spectrum data;

(3) determining (M3) a sequence of at least a portion of an oligomer from MSD, comprising:

(a) reading MSD in a first reading operation from a non-volatile storage device to a temporary volatile cache memory to obtain abundance values at a set of possible m/z values from the temporary volatile cache memory;

(b) calculating first abundance parameters from the abundance values, reading MSD in a second reading operation, following the first reading operation, from the temporary volatile cache memory to obtain the abundance values of the set of m/z values; and

(c) determining a ranking based on abundance values for each sequence of a set of monomer sequences having a first number of monomers; and

(4) processing (M4) MSD of extract specific labeled ions of interest, comprising determining a periodic block of noise in MSD generated from accelerating unlabeled ions to a detector and filtering the periodic block of noise from MSD.

USE - M1 is useful for deriving sequence of a portion of oligomer from MSD, where the oligomer is a protein, nucleic acid or oligosaccharide (claimed).

ADVANTAGE - M1 has the ability to sequence full proteins and nucleic acids without the need for prior digestion into small peptides or nucleic acids. The method is self-starting and does not require any knowledge of the parent ion size or composition to determine the sequence. The method has the ability to determine partial protein sequences from regions of a protein that may not contain ionizable amino acid residues.

Dwg.070

FS CPI EPI

FA AE; ICH

MC CFI: B04-C01; B04-C02X; B04-E01; B04-N04; B11-C08A; B11-C08E4; B12-K04;
 D05-H18A

EPI: S03-E10AS; S03-E14H5; T01-J08A2; V05-J01A

TECH OPTX: 20021010

TECHNOLOGY FOCUS - BIOTECHNOLOGY - Preferred Method: In M1, the oligomer from MSD of fragments is used. The second ranking is also calculated and the a cumulative ranking, based on first and second ranking, for each sequence of a set of fragment sequences having at least the second number of monomers is calculated. The terminal portion of the protein is a N-terminus, C-terminus and 3'terminus. The label which is attached to the terminal portion is covalently bonded to the protein to generate the mass spectrum data and the mass spectrum data is transformed from an output of a detector plate. The protein is fragmented by collision-induced dissociation to generate fragments, which are accelerated towards a detector plate to generate the mass spectrum data. The protein is isolated from other proteins extracted from a sample, where the method involves a digital processing system which executes computer programming instructions. PDS comprises all possible m/z values empirically found in mass spectra for all possible amino acid sequences having a number of amino acids from one amino acid to a selected number of amino acid, the selected number is in a range from 4-6 amino acid. PDS comprises a set of

fragments and a set of ionic charge states. The method is performed for each protein in a set of proteins extracted from a biological material and where the set of proteins are more than 100 different proteins. In M3, the first abundance parameters and the ranking for the sequence are stored in temporary volatile cache memory. The m/z values is calculated as needed rather than stored on a non-volatile storage device. The ranking for the sequence is determined from the first abundance parameters and the abundance values obtained in the second reading operation, and where the temporary volatile cache memory comprises at least one of an L1 and an L2 cache of a microprocessor. The label is covalently bonded to a primer sequence of a nucleic acid prior to the fragments being generated by Sanger, polymerase chain reaction, or Maxam-Gilbert methods and the generation of mass spectrum data. In M4, one or more labels are used. The label incorporates one or more elements with an atomic number between 17 and 77, excluding S and F. The mass defect elements of the label have an atomic number between 35 and 63.

ABEX

UPTX: 20021010

EXAMPLE - A high mannose type oligosaccharide was sequenced. The mass defect label 2-amino-6-iodo-pyridine (Label 1) was conjugated to the reducing terminus of the oligosaccharide in the presence of sodium cyanoborohydrin (NaBH_3CN). This incorporated a single mass defect element (I) into the parent oligosaccharide. The addition of the mass defect element allowed the labeled oligosaccharide fragments to be distinguished from unlabeled fragments and matrix ions in the mass spectrum. The label 1 conjugated oligosaccharide was then aliquoted. The reactions were allowed to proceed to completion. Upon completion, the reaction products were subsequently conjugated at the reducing ends of the fragments generated by reaction with the mass defect labels shown for each enzyme: alpha-mannosidase I, alpha-mannosidase, alpha-mannosidase II, beta-mannosidase, beta-hexosaminidase and N-acetyl beta-hexosaminidase in the presence of sodium cyanoborohydrin. Since these labels contain different numbers of mass defect elements, the digested fragments may be distinguished from the terminal fragment of the original oligosaccharide. An aliquot of the Label 3 conjugated reaction mixture (i.e. digested with enzyme alpha-mannosidase II) is further digested with enzyme 1. The reaction reducing sugar termini generated by this reaction were subsequently conjugated to Label 2. Aliquots from all these reactions were then mixed, acidified by the addition of a 50% v/v mixture of 1% acetic acid in methanol and subjected to mass spectral analysis. Alternatively, a different label series that incorporated a hard charge (e.g. an N-alkyl-iodo-pyridinium series) could be subjected to mass spectral analysis without acidification. The resulting mass spectrum was deconvolved to remove all chemical noise that does not contain a mass defect labeled peak. The resulting deconvolved mass defect spectrum was then algorithmically searched by predicting all the possible oligosaccharide sequences that could be attached to each mass defect label used. The search algorithm calculated the mass for every branch combination of hexose (Hex), and N-acetylaminohexose (HexNAc). The mass ladder formed the fragments conjugated to Label 1 suggested that the outermost sugars must be hexoses. Since the highest mass fragment conjugated to label 1 must correspond to the parent oligosaccharide, then it was deduced that the 4 hexose mass difference to the first label 1 conjugated fragment must correspond to 4 alpha-mannoses since both enzyme 1 and enzyme 3 only cleaved alpha-mannoses. The next fragment in the label 1 mass ladder differed by an addition 4 hexoses from the previous fragment. This must correspond to a sample digested with enzyme 2. The only matching label 3 conjugated fragments were hexose fragment, F (1-2 hexose fragment) and G (a 3 hexose fragment). Since peaks F and G total 5 hexoses, it was deduced that at least one of these fragments must contain a 1-6 linked mannose. Since enzyme 3 only cleaves 1-3 and 1-6 linkages, therefore it was further deduced that there must be at least two separate 1-6 linked mannoses in the structure and that these mannoses must be interior to the 4-1 alpha linked mannoses. From this information it was deduced the following

partial sequence: (Man4-1 alpha 2)-(HexNAc,Man-1 alpha 2,6)-(HexNAc2,Hex1)-r where r indicates the reducing end of the oligosaccharide. This process was repeated with different enzymes until the complete sequence was determined. For e.g. digestion with enzyme alpha-mannosidase II followed by enzyme beta-mannosidase allowed the determination that the initial sequence is: -Man-1 beta 4-(HNAc2)-r. The full sequence of the reducing end of the oligosaccharide was determined by reaction with enzyme alpha-mannosidase II followed by enzyme N-acetyl beta-hexosaminidase.

L90 ANSWER 3 OF 5 WPIN (C) 2003 THOMSON DEERWENT

AN 2002-426317 [45] WPIN

DNN N2002-335207 DMC C2002-120869

TI Determining mass of a mass altering group present in an assayed peptide and absent from a corresponding database peptide, or vice versa, involves creating mass spectrometry data and comparing it with sequence database.

DC B04 D16 S03 T01

IN SMILANSKY, S

PA (COMP-III) COMPUGEN LTD

CYC 97

PI WO 2002010884 A2 20020418 (200245)* EN 46p G01N033-63 ---

FW: AT PE CH CY DF DK EA ES FI FF GE GH GM GF IF IT KE LS LU NU MW NE
HL OA PT SD SE SL SS TF TS UG SW

W: AE AG AL AM AT AU AZ BA BE BG BF BY CA CH CN CO CR CU CE DE EK
DM EC EG EE ES FI GE GD GE GH GM HR HU ID IL IN IS JP KE KG KE KE
KS LC LE LF LS LT LU LV MA MD ME MF MN MW MX MC NG NE PH PL PT PQ
RU SD SE SG SI SK SL TJ TM TR TT TC UA UG US UC VN YU ZA SW

AU 2002010884 A 20020422 (200254) G01N033-68 ---

ADT WO 2002031509 A2 WO 2001-IL944 20011011; AU 2002010884 A AU 2002-10384
20011011

FET AU 2002010884 A Based on WO 200231509

PFAI IL 2000-138946 20001011

IC ICM G01N033-68

ICS C1L0001-37; G06F019-00

AB WO 200231509 A UFAB: 20020717

NOVELTY - Determining mass of a mass altering group present in an assayed peptide (AP) and absent from a corresponding database peptide (DP), and vice versa, involves treating AP with at least two digestion agents (DA) to produce products, each having many assayed fragments, obtaining mass values of the fragments, and comparing with theoretical masses of fragments obtained by treatment of DP with the respective two DA.

DETAILED DESCRIPTION - Determining (M1) mass of a mass altering group or identifying (M2) a cleavage altering sequence present in AP and absent from a corresponding DP, and vice versa, comprises:

(a) treating AP with a first DA to obtain a first digestion product comprising several first assayed fragments, and determining the mass spectrum of the digestion product to obtain one or more mass values of the individual first assayed fragments M1a;

(b) treating AP with a further DA to obtain a further digestion product comprising several further assayed fragments, and determining the mass spectrum of the digestion product to obtain one or more mass values of the individual further assayed fragments M1a;

(c) optionally repeating step (b) according to the number of different further DAs, obtaining mass values of the individual further assayed fragments M1a, M1a, M1a;

(d) optionally identifying AP, in case of a peptide not identified earlier, by a suitable protein identification method;

(e) obtaining masses M1a or M1a of the individual theoretical fragments of DP corresponding to AP, which fragments are obtained by the theoretical digestion of DP with the first or further DA;

(f) comparing each of M1a with each database value M1a, to obtain several differences Di = M1a-M1a and discarding all Di values lower than a predetermined threshold value to give several selected differences Di'; and

(g) comparing each of M_{ja} with each database value M_{jt} , to obtain several differences $D_j = M_{ja} - M_{jt}$ and discarding all D_j values lower than a predetermined threshold value to give several selected differences D_j' .

(M1) further comprises a step (h) of comparing selected differences D_i' and D_j' , preferably comprising overlapping theoretical fragments, and identifying those which are essentially identical, and optionally repeating steps (e)-(h), according to the number of different further DAs, obtaining selected differences $D_k'/D_l'/D_m'$, etc. The required mass of the mass altering group is defined by the essentially identical D_i'/D_j' values. (M2) comprises repeating step (e) according to the number of different further DAs, obtaining masses M_{kt} , M_{lt} , M_{mt} , etc., of the individual theoretical fragments. Step (f) and (g) involves discarding all M_{ia}/M_{ja} and M_{it}/M_{jt} for which at least one of the D_i/D_j values is lower than a predetermined threshold value and thus identifying orphan M_{ia}/M_{ja} that has no corresponding M_{it}/M_{jt} , and orphan M_{it}/M_{jt} that has no corresponding M_{ia}/M_{ja} . (M2) further comprises (after step (g)): (h) optionally repeating step (g) as above according to the number of different further DAs, and thus identifying orphan M_{ka} , M_{la} , M_{ma} , etc., that have no corresponding M_{kt} , M_{lt} , M_{mt} , etc., and identifying orphan M_{kt} , M_{lt} , M_{mt} , etc., that have no corresponding M_{ka} , M_{la} , M_{ma} , etc. (i) defining a first orphan region as the subset of the amino acid sequences of DP which includes all the theoretical fragments corresponding to orphan M_{it} for the first DA, defining a further orphan region as the subset of the amino acid sequences of DP which includes all the theoretical fragments corresponding to orphan M_{jt} for the further DA, optionally repeating this for further DAs M_{kt} etc., and finally defining a peptide orphan region as the intersection of the first orphan region with all further orphan regions, thus consisting of a subset of sequences of the peptide that were not identified by any of the DAs; (j) theoretically altering the amino acid sequence of the peptide orphan region, by adding, deleting or changing one or more amino acids, to obtain altered database fragments, and calculating a set of theoretical values of masses M_{alt} of the altered fragments; (k) comparing each M_{alt} with an orphan M_{ia} , orphan M_{ja} , orphan M_{ka} , etc., and selecting those M_{alt} of which the difference from an orphan M_{ia} , M_{ja} , M_{ka} etc., is smaller than a predetermined threshold value. M_{alt} representing the correct change is selected based on a pre-determined criterion, for e.g., confirmation by the largest number of different DAs, and thus identifying the amino acid sequence which is present only in AP or in DP as the altered database fragment contributing to the M_{alt} .

An INDEPENDENT CLAIM is also included for a kit for determining a mass altering group and/or cleavage altering sequence of a peptide for use with mass spectroscopy, comprising two or more DAs, unit for digesting peptides with the agents, and an instruction manual.

USE - (M1) is useful for determining the mass of a mass altering group e.g. a sugar group, lipidic group, acyl group, acidic group, flavin, pyridoxal phosphate, or a group added by oxidation of sulfur in the peptide, or an amino acid sequence of one or more amino acid residues present in AP and absent from corresponding DP, and vice versa. The mass of the mass altering group that was determined is used to determine the identity of the group. (M2) is useful for identifying a cleavage altering sequence present in AP and absent from a corresponding DP (claimed). (M1) and (M2) enable to characterize the type of the mass altering group and cleavage altering sequence, determining its mass, identity, as well as its location within the amino acid sequence.

Dwg. 0/4

FS CPI EPI

FA AB; DCN

MC CPI: P04-C02; B04-L05C; B04-N04; B04-N04B; B05-B01M; E06-A01; B11-C07A; B11-C08E1; B11-C08DL; B11-C08E; B11-C08E3; B11-C08E6; B12-K04; D05-A02C; D05-H09

EPI: S03-E14H; T01-J

TECH CPTX: 20010717

TECHNOLOGY FOCUS - BIOTECHNOLOGY - Preferred Method: DA is a chemical agent or a proteolytic enzyme, such as cyanogen bromide, trypsin, chymotrypsin, Glu-C, Lys-C, AspN, elastase or thermolysin. The amino acid sequence shared by the overlapping theoretical fragments is used to determine the identity and/or the location of the mass altering group within the amino acid sequence. In step (d), AP is identified by mass spectrometry, protein sequencing, immunoassay, chromatography, electrophoresis, protein chips or antibody chips. The predetermined threshold value is based on the experimental error of the methods and equipment involved. The essentially identical M_i/D_j values defining the mass of the mass altering moiety may differ according to the error of the methods and equipment involved. The difference between AP and DP is due to a difference in organism strain or species, due to a database error, single nucleotide polymorphism (SNP) or signal peptide cleavage. AP and DP comprise non-identical, homolog sequences. The mass altering group or the cleavage altered sequence results from a mutation, alternative splicing, RNA editing, a post-translational modification that occurred in vivo, or a modification that occurred in vitro during sample preparation. The post-translational modification comprises acetylation, amidation, deamidation, farnesylation, formylation, geranylation, hydroxylation, methylation, myristoylation, phosphorylation or sulfation.

Preferred Kit: The kit comprises at least two proteolytic enzymes.

UPTX: 20020717

ABEX

EXAMPLE - The assayed protein was identified by the standard methods as corresponding to database peptides (DPs) known as C0Q7Human having the sequence: KMWDQEKDHLKKEFELMVMFVRVEPTVLMELWNLGFAIGAGTALLG. The first DA was trypsin, which selectively cleaved at the C-terminus of R and K, not before P. Theoretical digestion produced 6 fragments K; MWDQEK; DHLK; K; FNELMVMF; VRPTVLMELWNLGFAIGAGTALLG. The masses of the theoretical database fragments (defined as M_i) were M_{i1} , M_{i2} , M_{i3} , M_{i4} , M_{i5} and M_{i6} , respectively. The second DA was chymotrypsin and the fragments generated were KMW; DQEKDHLKKE; NELMVMF; VRPTVLMELW; NVLGF; ALGAGTALLG. The masses of the theoretical fragments (defined as M_{jt}) were M_{jt1} , M_{jt2} , M_{jt3} , M_{jt4} , M_{jt5} and M_{jt6} , respectively. The assayed peptide (AP) was modified by a post-translational modification to have modification X attached to the third amino acid W. The actual AP was treated in one reaction vessel with trypsin and in the other reaction vessel with chymotrypsin. Both digests were analyzed by mass spectrometry. The mass spectrum of the trypsin digest showed: M_{ia3} , M_{ia4} , M_{ia6} and M_{iu} (standing for unknown). The masses M_{ia3} , M_{ia4} and M_{ia6} of the AP were substantially identical (i.e. the difference was below a threshold value) to M_{i3} , M_{i4} and M_{i6} of the DP. However, $M_{ia u}$ had a mass that did not correspond to any of the fragments of the DP. The mass spectrum of the chymotrypsin digest showed: M_{ja2} , M_{ja4} , M_{ja6} and $M_{ja u}$, the first three being substantially identical to the corresponding fragments M_{jt2} , M_{jt4} and M_{jt6} . Then, the two unknown masses $M_{ia u}$ and $M_{ja u}$ obtained by treatment with trypsin and chymotrypsin, respectively, were compared with each of the fragments, of the DP. $M_{ia u}$ was compared with M_{i1-6} masses of the DP theoretically treated with trypsin, whereas $M_{ja u}$ was compared with M_{jt1-6} of DP theoretically treated with chymotrypsin. It was found that: $M_{ia u} - M_{i3} = M_{ja u} - M_{jt1} = X$. Thus, X was considered to be significant, i.e., the mass of an altering moiety. Since M_{i3} and M_{jt1} each contributed to this identical difference giving the mass X, it was possible to determine the sequence of the fragment having a mass M_{i3} (MWDQEK), and the sequence of fragment having a mass M_{jt1} (KMW). The region overlapping in these two sequences was MW, and this was the sequence where the modification X was present.

L9C ANSWER 4 OF 5 WPIX (C) 2003 THOMSON LEFWEENT
 AN 2001-356050 [37] WPIX
 CF 2001-35604 [37]
 DIN N2001-258684 DMC C2001-110490
 TI Identification of associated cell signaling proteins

useful to indicate common signaling pathways, uses comparison values based on data representing physical properties to identify associated pairs of proteins.

DC B04-L04 S03

IN PELECH, S

PA (UPE-NO) UNIV BRITISH COLUMBIA

CYC 25

PI WO 2001038879 A2 20010331 (200127)* EN 90 G01N033-68 ---
 FW: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE TF

W: AG CA JP NZ ES

A2 2001016844 A 20010604 (200153) G01N033-68 ---

EP 1234187 A2 20020828 (200264) EN G01N033-68 ---

R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL PT SE TF

ADT WO 2001038879 A2 WO 2000-CA1378 20001117; AU 2001016844 A AU 2001-16844
 20001117; EP 1234187 A2 EP 2000-979297 20001117, WO 2000-CA1378 20001117

FDT AC 2001016844 A Based on WO 200138879; EP 1234187 A2 Based on WO 200138879

PFAI US 2000-216357P 20000705; CA 1999-2290335 19991119; CA 1999-2290204
 19991119

IC ICM G01N033-68

AB WO 2001038879 A UFAI: 20021031

NOVELTY - **Cell signaling** proteins that are associated are identified by comparing pairs of proteins using comparison values based on data representing physical properties of the proteins, and identifying pairs having comparison values satisfying a condition indicative of an association.

DETAILED DESCRIPTION - The method comprises: (a) producing and storing comparison values for each pair based on data values representing physical properties of the respective proteins; and (b) identifying pairs having comparison values satisfying a condition indicative of an association between the proteins.

INDEPENDENT CLAIMS are also included for:

(1) an apparatus for conducting the method, comprising a receiver operable to receive the data values, and a processor circuit in communication with the receiver and configured to produce and store in a memory the comparison values and identify pairs as above;

(2) a computer readable medium providing instructions to direct a programmable device to conduct the method as above; and

(3) a computer data signal embodied in a carrier wave comprising code segments to direct a programmable device to receive data values, produce and store comparison values and identify proteins pairs as in the method above respectively.

USE - The method is useful to identify associations between **cell signaling** proteins (e.g. **kinases**), useful to infer that the proteins form part of a common signaling pathway and so gain further information about such signaling pathways and networks.

Cell signaling proteins are important proteins which regulate expression and activity of proteins in cells, and operate within signaling pathways and networks which govern and coordinate all cellular functions e.g. cell metabolism or death.

ADVANTAGE - The method and apparatus can be used to measure a large number of **kinases** and **kinases** substrates in a single sample.

Dwg. 0/01

FS CFI EPI

EA AE; DCU

MC CFI: B04-H01; B04-L04; B11-C07B4; B11-C08B1; B12-K04A; D05-H09

EPI: S03-E14H

TECH UFTX: 20010704

TECHNOLOGY FOCUS - INSTRUMENTATION AND TESTING - Preferred Method: optionally, the method also comprises producing data values representing physical properties of the proteins e.g. by producing signals representative of proteins in a single dimensional electrophoreses gel. Data values are preferably normalized relative to at least one reference

value before producing comparison values, and comparison values are preferably produced and stored in a random access memory. Comparison values may be generated by: (i) receiving sets of data values representing amounts of respective **cell signaling** proteins in the biological material, and producing a coexpression coefficient for each pair, representing the degree of coexpression of the respective proteins of the pair; (ii) receiving sets of data values indicating the phosphorylation states of the respective **cell signaling** proteins in the biological material, and producing a coregulation coefficient for each pair, representing the degree of coregulation of the respective proteins of the pair; or (iii) combining the results of the coexpression and coregulation analysis to produce a linkage coefficient for each **cell signaling** protein pair, as a function of the coexpression and coregulation coefficients for the pair (e.g. by dividing coregulation coefficient by coexpression coefficient). Preferred methods for (i)-(iii) are detailed in the specification. Method (iii) optionally also comprises associating at least some of the **cell signaling** proteins with respective common signaling pathways in response to the linkage coefficients (preferred methods are detailed in the specification) and optionally producing lists of such common signal pathways. Identification as in (b) preferably comprises producing a list of: pairs of associated **cell signaling** proteins; clusters of associated **cell signaling** proteins (preferred method given in the specification); or clusters of pairs for which each member of each pair is present in at least one other pair of the group.

Preferred Apparatus: Preferably, the memory is integral, and the processor circuit is configured for preferred methods as above. Especially preferred apparatus is detailed in the specification. A measuring device which can produce the data values (e.g. a chemiluminescence imager producing signals from a single dimensional electrophoresis gel) is optionally included; electrophoresis apparatus (e.g. for sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE)) is optionally also included.

ABEX UPTX: 20010704

EXAMPLE - None given.

L90 ANSWER 5 OF 5 WPIX (C) 2003 THOMSON DERWENT

AN 2001-356049 [37] WPIX

CR 2001-356050 [37]

DNN N2001-258683 DNE C2001-110489

TI Detecting multiple groups such as kinases or kinase substrates in test sample, comprises separating proteins in sample to produce one-dimensional array, contacting array with antibodies and detecting antibodies bound to groups.

DC B04 D16 S03

IN PELECH, S

PA (UTRE-N) UNIV BRITISH COLUMBIA

CYC 25

PI WO 2001038877 A1 20010531 (200137)* EN G1p G01N033-573

FW: AT BE CH CY DE DK ES FI FR GE GR IE IT LU MC NL PT SE TF

W: AU CA JP NZ US

CA 2290335 A1 20010519 (200141) EN C12Q001-48

CA 2290204 A1 20010522 (200143) EN C12Q001-48

AU 2001016843 A 20010604 (200153) G01N033-573

EP 1234184 A2 20020828 (200264) EN G01N033-573

F: AT BE CH CY DE DK ES FI FR GE GR IE IT LU MC NL PT SE TF

AET WO 2001038877 A2 WO 2000-CA1377 20001117; CA 2290335 A1 CA 1999-2290335

19991119; CA 2290204 A1 CA 1999-2290204 19991122; AU 2001016843 A AU

2001-16843 20001117; EP 1234184 A2 EP 2000-079226 20001117, WO 2000-CA1377 20001117

FDT AU 2001016843 A Based on WO 2001038877; EP 1234184 A2 Based on WO 2001038877

PRAI US 2000-116357F 20000705; CA 1999-2290335 19991119; CA 1999-2290204 19991122

IC ICM C120001-48; G01N033-573
ICS C120001-42; G01N033-585
AB WO 200138877 A UFAB: 20021031

NOVELTY - Detecting (M) multiple groups such as kinases or kinase substrates in a test sample comprising:
(1) electrophoretically separating proteins in the sample to produce a one-dimensional array of proteins so separated;
(2) contacting the array with antibodies such as anti-kinase (substrate) antibodies; and
(3) detecting the presence of antibodies bound to kinase (substrate) groups in the array, is new.

USE - (M) is useful for detecting multiple groups such as kinases or kinase substrates in a test sample (claimed). (M) is useful for the discovery of new protein kinases, to detect unknown proteins which can cross-react with kinase-specific antibodies, and to identify known proteins and detect new proteins that may bind with high affinity to a target protein.

ADVANTAGE - (M) has many advantages over standard 2-dimensional (2D) gel proteomic methods. (M) can be applied to any cell or tissue samples, and no prelabeling with radioisotopes is necessary, because kinase detection is based on immunoreactivity. (M) can be adapted for wide scale diagnostic applications because patterns of protein kinase expression are stable for periods of up to six hours before an organ is stored during this time fractionation and freezing, providing the organ is stored during this time over ice. This procedure may be carried out within two days from start to finish when compared to the 2D gel electrophoresis which is extremely laborious, much more difficult to render and takes at least twice a time. (M) provides ability to compare multiple samples side by side, whereas the 2D gel can be used for a single sample. An advantage of (M) over other methods to examine protein-protein interactions such as the yeast two-hybrid method, is that it can detect interactions that are affected by the state of post-translation regulation of these proteins, such as their phosphorylation state.

Dwg. 0/0

FS CFI EPI

FA AB; DCU

MC CFI: E84-G03; B04-G21; P04-L04; B11-G07A; E11-G08D1; E12-K04A; D05-A01E;
D05-H09; D05-E11B

EPI: S03-E14E4

TECH UPTX: 20010704

TECHNOLOGY POINTS - PIOTECHNOLOGY - Preferred Method: (M) further comprises recording one or more values representative of location of antibodies bound on the array by measuring intensity of a signal representative of an amount of antibody at a location on the array and recording a value or values representative of the intensity. Recording comprises exposing photographic material to the array and developing the photographic material to produce a record, or scanning the array to produce a record comprising a signal. The signal comprises a data structure consisting of the values, and the signal is stored in a machine readable medium. In (M), at least one protein phosphatase is added to the sample prior to separating to dephosphorylate proteins in the sample, and at least one protein phosphatase is inactivated prior to separating. At least one kinase and adenosine triphosphate (ATP) is added to the sample to phosphorylate substrates of the added kinase prior to separating, and the added kinase is inactivated prior to separating. Separation is done in a sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) gel in a single dimension, where the proportions of acrylamide and bisacrylamide in the gel are selected to permit separation of phosphorylated and non-phosphorylated states of a single kinase or kinase substrate group. The proteins electrophoretically separated exclude proteins from the sample of less than about 25 kilo dalton (kD). In (M), at least one of the antibodies comprises a polyclonal antibody mixture, and the array is transferred to a membrane prior to contacting with

antibodies. Detection comprises monitoring the presence of an antibody selectively bound to anti-kinase (substrate) antibodies, where an enzymatic reaction catalyzed by a group conjugated to the antibody selectively bound to anti-kinase substrate antibodies is monitored.

UPTX: 00010704

ABEX

EXAMPLE - The presence of over 45 different protein kinases in soluble extracts prepared from the whole brain, heart and skeletal muscle of adult male Sprague-Dawley rats was probed. The results demonstrated large differences in kinase expression patterns between these tissues. Brains, hearts and hind leg tibial skeletal muscles from 50 day old male Sprague-Dawley rats were rapidly excised. The tissues were cut, rinsed with phosphate buffered saline, frozen in liquid nitrogen, and stored. The tissues were pulverized, re-suspended in ice-cold homogenization buffer and sonicated. The homogenates were ultracentrifuged and the supernatants were immediately frozen until subsequent analysis. The thawed cell lysates were measured for protein content using Bradford reagent with bovine serum albumin as the reference standard. The protein concentration of the lysates was adjusted to 1 mg/ml in sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) sample buffer and boiled. 1 mg of the cell lysate was loaded on to the stacking layer of an SDS-PAGE gel. Electrophoresis was performed until proteins of 25,000 Daltons had migrated to the bottom of the gel. Proteins were then electrophoretically transferred from the gel on to a nitrocellulose membrane, and the membrane was subsequently cut vertically into 1 cm wide strips. The strips were then blocked with 5% skim milk powder in Tris-buffered saline and, after quickly rinsing the membrane with TBST (undefined), each strip was exposed to a unique mixture of different primary antibodies in TBST. The strips were washed with TBST and incubated with horseradish peroxidase-conjugated secondary antibody. After washing the strips with TBST, the strips were reassembled, and subjected to the enhanced chemiluminescence (ECL) Western blotting detection system. The results showed that the patterns of kinase expression differed markedly between the tissues. At least 45 known protein kinases were visualized on the immunoblots and clearly identified based on their predicted sizes and immunoreactivities.

=> d his

(FILE 'HOME' ENTERED AT 10:00:35 ON 28 MAY 2003)
SET COST OFF

FILE 'MEDLINE' ENTERED AT 10:00:57 ON 28 MAY 2003
E PELECH S/AU

L1	151 S E3-E7
L2	51 S L1 AND L1./CT
	E CELL COMMUNICATION/CT
	E E3+ALL
L3	13501 S E4
L4	73012 S E22
L5	135619 S E4+NT
	E E30+ALL
	E SIGNAL/CT
	E E52+ALL
L6	73012 S E11
L7	120317 S E11+NT
L8	40 S L1 AND L2-L7
L9	73 S L1 NOT L2,L3
L10	73 S L2,L3

FILE 'HCAPLUS' ENTERED AT 10:34:17 ON 28 MAY 2003
E PELECH S/AU

L11	100 S E3-E9
L12	2 S L11 AND P/DT

```

E INFORMATION SYSTEMS/CT
L13 6662 S E3,E8,E9,E10,E19-E21,E23,E25-E27
L14 6662 S E3-E27
      E E3+ALL
L15 11394 S E2-E7
L16 6916 S E24-E47
      E E68+ALL
L17 3947 S E1
      E MEMORY DEVICE/CT
L18 7213 S E29-E31
L19 3570 S E9
      E E4+ALL
L20 43101 S E4+NT
L21 338 S L13-L17 AND L18-L20
      E SIGNAL TRANSDUCTION/CT
      E E6+ALL
L22 2 S L21 AND E1+NT
      E E8+ALL
L23 1 S L21 AND E4+NT
L24 77 S L21 AND (FIOCHEM?(L)METHOD?)/SC,SX
L25 25 S L21 AND SIGNAL?
      E PHYSICAL PROPERT/CT
L26 2 S L21 AND E4
L27 52 S L21 AND PROTEIN
L28 4 S L12,L22,L23,L26
L29 24 S L24,L25 AND L27 NOT L28
L30 80 S L24,L25,L27 NOT L28-L29
      SEL DN AN 12 13 16 18 80 82
L31 6 S L30 AND E1-E18
L32 10 S L28,L31
L33 24 S L29 NOT L30-L32
      SEL DN AN 7 8 10 11 14 19
L34 6 S L33 AND E14-E26
L35 10 S L32,L34 AND L11-L34
      E MATHEMATICAL METHOD/CT
      E E4+ALL
L36 98747 S E3-E5,E2+NT
      E E123+ALL
L37 36824 S E2,E1+NT
L38 150770 S E9+NT OR E14+NT OR E15+NT OR E16+NT
L39 92 S L21 AND L36-L38
L40 11 S L39 AND L35
L41 16 S L35,L40
L42 30 S L39 NOT L29-L35,L41
L43 16 S L41 AND L11-L42

```

FILE 'HCAPLUS' ENTERED AT 11:00:09 ON 28 MAY 2003

```

L44 9 S L21 AND CLUSTER?
L45 8 S L44 NOT L43
      SEL DN AN 2 3
L46 6 S L45 NOT E1-E6
L47 6 S L46 AND L11-L46

```

FILE 'COMPUSSIONCE' ENTERED AT 11:04:19 ON 28 MAY 2003

```

E FELECH/AU
E RANDOM ACCESS/CC
E MEMORY/CC
L48 5527 S E3
      E RANDOM ACCESS/ST
L49 3061 S RANDOM?/ST
L50 110 S L48 AND MEMOR?/CC,ST
L51 0 S L50 AND (PROTEIN OR PEPTIDE OR POLYPEPTIDE OR NUCLEIC ACID OR
L52 6 S L48 AND (PROTEIN OR PEPTIDE OR POLYPEPTIDE OR NUCLEIC ACID OR

```

SEL DN AN 6
1 S L52 AND E1

L53

FILE 'COMPUSCIENCE' ENTERED AT 11:08:09 ON 28 MAY 2003

L54 76 S MEMORY DEVICES/ST
L55 5527 S MEMORY/CC
L56 5530 S L54,L55
L57 6 S L56 AND (PROTEIN OR PEPTIDE OR POLYPEPTIDE OR NUCLEIC ACID OR
L58 11 S L56 AND CELL? (L) SIGNAL?
L59 11 S L57,L58 NOT L52

FILE 'COMFUAB' ENTERED AT 11:09:59 ON 28 MAY 2003

E MEMORY/CC
E BIO/CC
L60 8711 S E4-E27
L61 204 S L60 AND MEMOP?
L62 12 S L61 AND RANDOM?
L63 2694 S RANDOM? ACCESS?
L64 11 S L63 AND L60
L65 7 S L64 NOT L62
L66 1624 S L63 AND STOR?
L67 211 S L66 AND SIGNAL?
L68 2 S L60 AND L67
L69 37 S L67 AND CELL?

FILE 'WEIK' ENTERED AT 11:14:05 ON 28 MAY 2003

E PELECH S/AU
L70 4 S E3
SEL DN AN 1 2
L71 2 S L70 AND E1-E6
L72 7137 S G01NC33-68/IC, ICM, ICS
L73 1064 S L72 AND (M424 OR M740)/M0,M1,M2,M3,M4,M5,M6
L74 854 S L73 AND (N102 AND N233)/M0,M1,M2,M3,M4,M5,M6
L75 276 S L73 AND (N102 AND N136)/M0,M1,M2,M3,M4,M5,M6
L76 408 S L73 AND (N102 AND N135)/M0,M1,M2,M3,M4,M5,M6
L77 845 S L74-L76
L78 21 S L77 AND G06F/IC, ICM, ICS
L79 21 S L77 AND T3/MC
L80 21 S L77 AND T3/EC
L81 0 S L77 AND G06T/IC, ICM, ICS
L82 715 S L77 AND S03/DC
L83 705 S L77 AND S03-E14H?/MC
L84 18 S L82,L83 AND CELL? SIGNAL?
L85 41 S L82,L83 AND ?KINASE?
L86 13 S L82,L83 AND (204-L04 OR C04-L04)/MC
L87 2 S L82,L83 AND (E04-E02C4 OR C04-E02C4)/MC
L88 85 S L71,L78-L80,L84-L87
SEL DN AN 17 19 28 34
L89 4 S L88 AND E7-E18
L90 5 S L71,L89 AND L70-L89

FILE 'WEIK' ENTERED AT 11:26:49 ON 28 MAY 2003
SEL DN AN L71

FILE 'WPCI' ENTERED AT 11:27:36 ON 28 MAY 2003

L91 0 S E13-E24